
ITEMS FROM THE UNITED KINGDOM**JOHN INNES CENTRE****Norwich Research Park, Colney Lane, Norwich NR4 7UH, United Kingdom.*****Genetics of adult plant resistance to yellow rust.***

Lesley Boyd, Phil Smith, and Clare Lewis (née Ellerbrook).

Adult plant resistance to yellow rust is being examined in a number of wheat cultivars, including the U.K. cultivars Claire and Buster. In the South African wheat, Karioga, two major yellow rust-resistance QTL have been identified, one on chromosome 2B and the other on 7DS. The QTL on 7DS is believed to be the durable source of yellow rust resistance, *Yr18*.

Novel sources of resistance to biotrophic fungal pathogens.

Lesley Boyd, Phil Smith, and James Melicher.

The biology and genetics of developmentally regulated resistance to rusts and powdery mildews is being examined through a study of wheat mutants that express enhanced resistance to one or more of these pathogens. Mutants, isolated from the wheat varieties Hobbit 'sib' and Guardian, are being mapped to determine the number, location, and effect of each mutation contributing to each pathogen resistance. These mutant lines also are being assessed to determine their value as a source of resistance in U.K. breeding programs.

Effects of preinoculation light quantity on yellow rust infection.

Lesley A. Boyd, and Ruth McCormock.

A new program will look at the effects on preinoculation light levels on the ability of yellow rust to infect wheat. Preliminary studies indicate that high levels of light, before inoculation, induce a factor in the plant that aids the pathogen in its ability to infect. The aims of this program are to identify this plant factor and identify genetic variation for the levels of this factor produced by wheat.

The detection of QTL for lodging resistance in wheat.

Vinesh Verma, Liz Sayers, Lesley Fish, and John Snape.

Lodging is a major constraint to increasing yield in many crops but is of particular importance in the small-grained cereals. The genetic control of lodging and component traits in wheat was investigated through the detection of underlying QTL. The analysis was based on the identification of genomic regions which affect various traits related to lodging resistance in a population of 96 DH lines of the cross 'Milan/Catbird', mapped using 126 microsatellite markers. Field experiments measured lodging behavior under natural climatic conditions, but glasshouse tests also were conducted on the physical characteristics of the stem and root mass. The co-location of QTL allowed physiological traits measured in the glasshouse and field to be related to lodging under normal field conditions.

Although major genes related to plant height (*Rht* genes) were responsible for increasing lodging resistance in this cross, several other traits independent of plant height were shown to be important such as root and shoot traits and various components of plant yield. Yield components, such as grain number and weight, were shown to be an indicator of plant susceptibility to lodging. QTL for lodging and associated traits were found on chromosomes 1B, 1D, 2B, 2D, 4B, 4D, 6D, and 7D. QTL for yield and associated traits were identified on chromosomes 1B, 1D, 2A, 2B, 2D, 4D, and

6A. These results show that selection for lodging-resistant genotypes can be done via indirect selection based on the morphological traits of plant height and culm stiffness before flowering. In the population here, the most efficient way to improve lodging resistance would be a combination of indirect selection on plant height, combined with MAS on other, less easy to measure, physiological traits.

WGIN: The Wheat Genetic Improvement Network.

Robert Koebner, John Snape, Christian Rogers, Leodie Alibert (JIC); and Kim Hammond-Kosack, Peter Shewry, and Andy Phillips (Rothamsted Research).

WGIN is a new venture, funded by the U.K. Government Department for Environment, Food & Rural Affairs, as a 5-year initiative that started in July 2003. The two research partners (John Innes Centre (JIC) and Rothamsted Research (Rres)) will collaborate to provide a suite of underpinning resources and research to the U.K. wheat-breeding industry.

The JIC contribution involves (1) the provision and enhancement of germ plasm, taking in cultivar and landrace collections, cytogenetic stocks, and mapping populations; (2) the development of novel genetic markers, particularly aimed at genic sequences and will include platforms based on SSRs, SNPs, and functional DNA fingerprinting; (3) the incorporation of both markers and selected phenotypic traits of value to the enhancement of agricultural sustainability into genetic maps; (4) the linking of the physical and genetic maps of wheat by mapping ESTs onto a hexaploid wheat BAC library; (5) the analysis of the molecular diversity of U.K. and European winter wheats to illuminate the genetic basis of 50 years of genetic advance; and (6) the generation, maintenance, and characterization of a large collection of mutagenized lines to aid in gene discovery.

The RRes contribution focuses on (1) the use of the diploid wheat *T. monococcum* (AA genome) as a model system to identify novel sources of resistance to major U.K. pathogens with a nonbiotrophic life-style, i.e., Septoria leaf blotch, Tapesia eyespot, Fusarium ear blight, and soilborne cereal mosaic virus and its vector *P. graminis*, and to develop linked markers with which to screen diverse hexaploid collections; (2) PCR tilling to explore, in a high throughput manner, the diversity that naturally resides at specific loci or which has been generated through EMS mutagenesis (This technique will be applied only to genes of known biological significance, and both diploid and hexaploid wheat genotypes will be explored. A demonstration project will be established to identify variation in genes known to control preharvest sprouting, plant height, and plant defence signalling/disease resistance to multiple pathogens in other plant species); and (3) trait identification. The selected mapping populations, their parents, and selected genotypes from the diversity screen will be subjected to field trialing to analysis for specific trait characteristics. A highly focussed list of traits to be evaluated is decided by the management team each year. In years 1–3, traits under investigation include nitrogen use efficiency, the influence of canopy architecture on Septoria leaf blotch and Fusarium ear blight diseases, and various grain quality parameters. A searchable traits database will be established and all preëxisting traits data sets archived appropriately.

The Network is guided by a management committee which includes representatives from the funding agencies, the research providers, and the end-user community. The core project will provide genetic and molecular resources for research for a wide range of wheat research projects in the U.K. An annual stakeholders forum is held to facilitate liaison between the U.K. research and end user communities. Further details of all WGIN activities and contact details are located on the WGIN website (<http://www.wgin.org.uk/>).

Genetic diversity in wheat landraces.

Leodie Alibert, Christian Rogers, Pauline Stephenson, and Robert Koebner.

The JIC curates the Watkins wheat collection, which consists of ~900 hexaploid accessions collected worldwide in the 1920s and 1930s. As part of the WGIN project, we are generating single-plant progeny stocks for four individuals/accession, because intra-accession heterogeneity is frequent at the morphological level. Archive DNA has been collected from these selections by leaf squash on to Whatman FTA cards, and these DNAs will be used to SSR-genotype the materials to give an overview of the inter- and intra-accession diversity of the materials. These data will form the seed of a growing database record, which is intended to be internet available and searchable.

Molecular outcomes of variation in mutagenic pressure in wheat.

Nicola Hart and Robert Koebner (JIC) and Peter Jack and Richard Summers (Monsanto UK Ltd).

In this new project supported by Monsanto U.K., we are seeking to investigate the relationship between the intensity of mutagenesis and the size, nature, and frequency of induced genetic lesions in wheat. We are targeting initially the *rht* loci by mutagenizing (with γ - and x-ray) the tall, spring wheat cultivar Paragon with a range of mutagen load from below to well above the generally used dose of 250 Gy. The outcome of the mutagenesis will be monitored by analysis of a suite of amplicons covering the *rht* locus, exploiting both size discrimination (for deletions) and heteroduplex analysis (for sequence changes).

Homoeologous gene silencing in polyploid wheat.

Andy Bottley and Robert Koebner.

This project builds on the work reported last year (Ann Wheat Newslet **49**:161) in which comparisons were made between the SSCP profiles of gDNA and cDNA, to demonstrate the occurrence of silencing at some expressed sequence loci. We are extending the analysis to a larger sample of single copy EST loci, many of which have been derived from the NSF EST database. The analysis will be enabled by our acquisition of a WAVE dHPLC platform, which will generate greater resolving power than SSCP.

Genetic erosion in European winter wheat.

Simon Orford and Robert Koebner (JIC); Martin Ganai and Markus Wolf (Traitgenetics, Gatersleben, Germany); and John Law and James Reeves (NIAB, Cambridge, UK).

As part of a wider effort involving barley, potato, and maize, the EU FP5-funded Gediflux project has been involved in the collection of genotype data covering a collection of ~300 winter wheat cultivars, which represent the bulk of area sown in northern Europe in the period since 1945 and the ~200 National List cultivars (those which are legally traded). The overall collection has been typed at 42 SSR loci (one per chromosome arm), ~70 SSAP loci (derived from a retro-transposon LTR motif), and ~50 NBS fingerprint loci. Attention is now focussed on SNP genotyping. The final size of the dataset will exceed 100,000 data points, sufficient to closely model trends in diversity over time in European winter wheat. This project follows similar smaller-scale pilot projects in U.K. wheat and barley, which have been published in *Theoretical and Applied Genetics* **100**:912 and **106**:550, respectively.

The genetic basis of resistance against Fusarium and other facultative pathogens of winter wheat.

Paul Nicholson, Andrew Steed, Natalie Chapman, Nicolas Gosman, Richard Draeger, Elizabeth Chandler, Martha Thomsett, and Duncan Simpson.

As part of a continuing study of FHB resistance, the resistance of Arina and WEK0609 has been analyzed by spray inoculation of DH populations. Mapping and QTL analysis of resistance also continues, and skeletal genetic maps of these populations have been produced. Single-chromosome substitution lines of WEK0609 have been produced, and three chromosomes conferring resistance have been identified. A collaborative project is underway to assess the level of FHB resistance among U.K. wheat cultivars and to introduce and pyramid FHB-resistance genes from diverse sources to improve the level of resistance among winter wheat varieties in the U.K.

The resistance of *T. macha* 4A, previously reported, has been investigated further in single-chromosome recombinant DH lines. Resistance on this chromosome appears to be conferred by a single gene. The resistance is primarily of type 1 and leads to reduced symptoms and accumulation of DON mycotoxin. In addition, mapping and molecular studies of two eyespot resistance genes (*Pch1* and *Pch2*) is also being undertaken.

Molecular diagnostics (species-specific competitive PCR) are being used to study interactions between spike and stem base disease pathogens on different cereal hosts. This work is combined with continued development of molecular diagnostics to determine the chemotype of individual isolates of *Fusarium* species for use in epidemiological studies.

Web access to passport data relating to wheat germ plasm resources at JIC.

Mike Ambrose and Steve Reader.

Wheat Precise Genetic Stocks (WPGS). A concerted program of database development and record entry relating to these resources has been ongoing for the past 2 years. At present, this data is available as a Microsoft Word-based files via the JIC Web pages (http://www.jic.ac.uk/GERMPLAS/prec_ce/index.htm). A searchable web interface is under development and should soon be operational.

The Crop Genetics Department at JIC has accumulated a large collection WPGS over the last 60 years. Many are the products of research programs at both the JIC and the former Plant Breeding Institute in Cambridge, U.K. Other lines were donated freely by fellow scientists from around the world. This extended collecting period has meant that often original donors have retired or may no longer be alive. Similarly, cultural and political trends within originating countries have occasionally compromised the viability of material, such that JIC may be one of the very few sources remaining.

The collection includes the late Ernie Sears collection of aneuploids in the cultivar Chinese Spring and lines which have a pair of chromosomes from a related species added to the wheat complement, a pair substituted for their wheat homoeologues, or a pair translocated with them. Also held are numerous amphiploids, stocks that contain the total complement of both parents. The work of the late Tony Worland is represented by 23 complete or partial monosomic series and several hundred derived, intervarietal substitution lines. These lines currently are being classified and entered into the database. However, many stocks are over 20 years old, and the primary concern currently is regenerating as many as possible each year to ensure that viable stocks will exist in the future. In due course, the Crop Genetics Department's collection of wheat landraces, wheat ancestors, and related species, also will be similarly accessible.

BBSRC Small Grain Cereal Collections. A searchable web interface is now available that enables users to interrogate passport data for the collections that include the public collection of some 9,500 wheat accessions (<http://data.jic.bbsrc.ac.uk/cgi-bin/germplasm/cereals.asp>). The user form offers the facility to select specific species and subspecies, country of origin, and status. Records can be sorted either by accession number or name. Individual record details are still under development but already include all available pedigree data.

Plant transformation facility for the U.K. research community.

Wendy Harwood, Judith Irwin, and John Snape (JIC); and Huw Jones (RRes).

The ability to genetically modify crop plants is an essential part of many research programs that contribute to the understanding and improvement of UK crops. Therefore, the availability of reliable genetic modification technology is of great importance to both basic and applied U.K. crop research.

BRACT (Biotechnology Resources for Arable Crop Transformation) is a U.K. Department for Environment, Food and Rural Affairs funded project that aims to make efficient transformation technology for the main U.K. crops available to the U.K. research community. The project was set up jointly between the John Innes Centre and Rothamsted Research and initially focuses on wheat, barley, and oilseed rape. The resources developed during the BRACT project will be tailored to meet the needs of the U.K. research community and will particularly concentrate on providing precise, efficient, and robust transformation technology that takes account of the current concerns over the use of GM crop plants.

The main transformation methodology used by the BRACT facility will be *Agrobacterium*-mediated transformation because this method leads to lower transgene copy numbers and more stable transgenic lines. The development

of 'clean-gene' transformants, where the selectable marker has been segregated away from the gene of interest, is an important part of the project together with the development of a new set of transformation vectors that will allow easy manipulation and insertion of genes of interest. As well as providing transformation technology and vectors, BRACT will provide assistance with crop transformation ranging from advice and training through to a complete transformation service.

Further information on the BRACT project can be found on the project website <http://www.bract.org/>.

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UNIVERSITY OF LEICESTER**Department of Biology, University Road, Leicester LE1 7RH, United Kingdom.****<http://molcyt.com> or <http://www.le.ac.uk/biology/phh4/index.htm>*****The 120-bp repeat family in diploid and polyploid Triticeae: its distribution, organization, evolution, and diversity.***

Alessandra Contento, J.S. Heslop-Harrison, and Trude Schwarzacher.

About 90 members of the 120-bp, tandemly repeated DNA sequence family originally described in rye as pSc119.2 sequence have been isolated from 11 diploid and polyploid Triticeae species using various primers for PCR amplification. Sequence homology and similarity analysis showed that the 120-bp repeat unit family is diverse with single nucleotide changes and a few indels occurring throughout the sequence. No characteristic genome or species-specific variants have developed during the evolution of the Triticeae species. Fluorescent *in situ* hybridization verified that the repeat is present as large blocks at mainly subtelomeric or interstitial sites in rye and the B genome of wheat and only has a few sites in the A and D genome of wheat. In all species investigated, each of the chromosomal sites harbored many different family members. Substantial copy number differences between genomes were observed, with the family being abundant in the R and B genomes but not A and D genomes. We conclude that homogenization events have not been operative in this repeat and that the common ancestor of the Triticeae tribe had multiple sequences of the 120-bp family with a range of variation not unlike that seen within and between species today. This diversity has been maintained when sites are moved within the genome and in all species since their split within the Triticeae.

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ITEMS FROM THE UNITED STATES OF AMERICA

COLORADO

COLORADO STATE UNIVERSITY

Department of Soil and Crop Sciences, Ft. Collins, CO 80523, USA.

Wheat breeding and genetics.

S. Haley, J. Stromberger, B. Clifford, S. Clayschulte, F. Pardina-Malbrán, J. Butler, and M. Collins.

Production conditions, test sites, and cultivar distribution. Total winter wheat production in 2003 was estimated at 77.0×10^6 bu, a 112 % increase from the disastrous 2002 crop but still 4 % lower than the 10-year average. Average grain yield, at 35.0 bu/acre, was 59 % higher than in 2002 and 4 % higher than the 10-year average. The area harvested for grain was estimated at 2.2×10^6 acres, up from 1.65×10^6 acres in 2002.

In 2002–03, the breeding program conducted field trials at four main locations in eastern Colorado (Akron, Burlington, Julesburg, and Walsh) in addition to the main location at the ARDEC research facility near Fort Collins. Overall, environmental conditions experienced at these locations can be described as follows: Akron – adequate yet less than optimal stands from poor planting moisture. Fairly dry winter, very wet spring and early summer. Very high level of stripe rust infection along with leaf rust in entries with good stripe rust resistance. Significant lodging. Very moderate temperatures until the last 10 days before harvest. Very high yields despite stripe rust; Burlington – poor autumn stands resulted from uneven moisture, stands filled in considerably with late autumn and early spring moisture. Fairly dry winter, good early spring moisture, and significant drought stress in May. Good moisture in June saved the trials. Very moderate temperatures until the last week before harvest. No significant disease or insect problems; Julesburg – excellent autumn stands, dry winter, adequate spring moisture, significant dry period around heading, adequate June moisture. Low levels of stripe rust and leaf rust. Some lodging observed. Moderate temperatures until the last 10 days before harvest. Very high yields, though limited by inadequate nitrogen availability (reflected in low grain protein); Walsh – excellent autumn stands, no winter injury, fairly dry winter, adequate early spring moisture, significant dry period from jointing through heading, severe (30–70 % damage) hailstorm 2 weeks after heading in early June, a second significant hailstorm 2 days before harvest. Moderate RWA observed, most likely biotype B based on susceptible reaction of RWA-resistant cultivars; Fort Collins (irrigated) – good autumn stands and moisture. Excellent spring growth, good spring rains reduced need for irrigation. Low levels of stripe rust and leaf rust. Significant RWA observed, most likely biotype A based on reaction of resistant cultivars. Significant lodging observed. Very moderate temperatures until the last 2 weeks before harvest.

In coöperation with the CSU Variety Testing Program under the direction of CSU Extension Agronomist Dr. Jerry Johnson, cultivars and experimental lines were tested at six other dryland trial locations (UVPT – Bennett, Cheyenne Wells, Genoa, Lamar, Orchard, and Sheridan Lake) and two other irrigated trial locations (IVPT – Ovid and Rocky Ford). Overall, both the dryland UVPT and the irrigated IVPT were a drastic improvement over 2002 as a good range of production conditions and yield levels were experienced. Of the total of 10 UVPT locations, four locations were either not harvested or were not used for the overall cultivar summary due to production conditions that prevented reliable data interpretation. The Genoa location was adversely affected by a severe hailstorm near the heading growth stage. The trial at Bennett did not emerge in the autumn, only partially emerged following the 17 March snowstorm, and stands remained highly variable. The Lamar and Sheridan Lake UVPT locations were characterized by uneven emergence, severe spring drought, multiple damaging hailstorms, and extremely low and variable yields. Both the Rocky Ford and Ovid IVPT locations were successfully harvested, although yields at the Ovid location were severely affected by stripe rust, perhaps surpassing the level observed in 2001. Very little virus (e.g., barley yellow dwarf or wheat streak mosaic) infection was observed at any of the testing locations. Russian wheat aphid was observed at higher levels than in recent years at several trial locations. Leaf rust was observed at very low levels at some locations, although at Akron it may have affected yields in those entries that had managed to maintain their leaves in response to the severe stripe rust infection.

Planted acreage estimates for the 2003 crop were as follows: Akron – 22.3 %; Prairie Red – 16.0 %; TAM 107 – 13.0 %; Jagger – 7.7 %; Above – 3.8 %; Yumar – 3.6 %; Lamar and Trego – 3.3 %; Prowers 99 – 2.6 %; Halt – 2.4 %; TAM 110 – 2.3 %; Alliance – 1.8 %; Platte – 1.5 %; Prowers, Yuma – 1.3 %; and other – 13.8 %.

Elite lines on increase. No new cultivars were released in autumn 2003. In September 2003, however, three experimental lines were put on foundation seed increase for potential release in 2004. The first of these lines, **CO980607** (Yuma/T-57//TAM 200/3/4*Yuma/4/KS91H184/Vista pedigree), would be positioned as a higher-yielding replacement for RWA-resistant (biotype A) cultivars including Stanton (from Kansas State), Prairie Red, and Yumar. CO980607 is an awned, white-chaffed, medium maturity, semidwarf HRWW. CO980607 is moderately resistant to stem rust, moderately susceptible to leaf rust, moderately resistant to stripe rust, susceptible to both wheat streak mosaic virus and barley yellow dwarf virus, and resistant to biotype A of RWA. CO980607 was the highest performing entry in the 2003 Colorado UVPT and had the second highest yield in the Southern Regional Performance Nursery (SRPN) across a six-location average of western Great Plains testing locations. Averaged across 17 trial locations of the dryland Colorado UVPT between 2001 and 2003, CO980607 (45.9 bu/acre) yielded slightly less than Trego (47.2 bu/a) but greater than all other entries in the trial, including Stanton and Enhancer (45.0 bu/acre), Above (44.5 bu/acre), Yuma and Alliance (44.3 bu/acre), Ankor and Jagger (41.5 bu/acre), Akron (43.7 bu/acre), Prairie Red (43.0 bu/acre), Halt (42.8 bu/acre), Yumar (42.4 bu/acre), and Prowers 99 (41.1 bu/acre). Average test weight of CO980607 in these trials (58.4 lb/bu) was lower than those of Prowers 99 (59.5 lb/bu) and Trego (59.8 lb/bu), similar to that of Yumar (58.3 lb/bu), and greater than that of Prairie Red (57.5 lb/bu). Milling and bread baking characteristics of CO980607 were determined from field-grown samples from the 2000, 2001, and 2002 seasons. Overall, CO980607 is characterized as having excellent milling properties and average to slightly better than average baking properties. CO980607 was entered for a second year of testing in the 2004 SRPN and for evaluation in the 2003-crop Hard Winter Wheat Quality Council (HWWQC). Approximately eight acres of CO980607 were planted in Colorado in the autumn of 2003 for Foundation Seed production.

The second line on increase, **CO00D007** (Yumar//TXGH12588-120*4/FS2 pedigree), is an awned, white-chaffed, medium-early maturity, tall semidwarf HRWW. CO00D007 is a *Clearfield*TM wheat that has shown dryland yields comparable to Above, improved baking quality characteristics, and resistance to biotype A of RWA. CO00D007 is about 1 day later at heading and 2 inches taller compared to Above. The straw strength of CO00D007 is slightly less than that of Above, similar to that of Akron. CO00D007 was the second highest performing entry in the 2003 Colorado UVPT across a six-location average. Across nine trial locations of the dryland Colorado UVPT during 2002 and 2003, CO00D007 (47.2 bu/a) yielded less than CO980607 (48.0 bu/acre) but greater than all other entries in the trial, including TAM 111 (46.8 bu/acre), Above and Trego (46.7 bu/acre), Ankor (45.8 bu/acre), Yuma (45.3 bu/acre), Prairie Red (45.0 bu/acre), Yumar (43.8 bu/acre), and AP502 CL (43.5 bu/acre). Average test weight of CO00D007 from these trials (58.4 lb/bu) was about 1 lb/bu lower than the trial average, lower than those of Above (59.0 lb/bu) and Yumar (59.3 lb/bu), and similar to that of AP502 CL (58.6 lb/bu). Milling and bread baking characteristics of CO00D007 were determined from a composite of field grown samples from both the 2001 and 2002 field seasons. Overall, CO00D007 is characterized as having slightly below average milling properties and better than average baking properties (especially when compared to Above), in spite of its lower protein and bake water absorption. In autumn 2003, a large Foundation Seed increase (20 acres) of CO00D007 was planted in Colorado. As a backup, a smaller increase (5 acres) of CO00D007 was planted in Yuma, Arizona. CO00D007 also was entered for regional testing in the 2004 SRPN and for evaluation in the 2003 crop HWWQC.

The third line on foundation seed increase, **CO991132** (Jagger//TXGH12588-120*4/FS2 pedigree), is a *Clearfield*TM wheat that shows distinct visual similarity to Jagger. CO991132 did not perform as well as Above or CO00D007 in Colorado but appeared to show promise in other areas of the Great Plains, particularly in Kansas where it outperformed Jagger by 5 bu/acre and the new Kansas State release Overlay by 2 bu/acre on a four location average. CO991132 has shown better baking quality scores than Above, but not quite as good as the Jagger parent. In autumn 2003, a 10-acre foundation seed increase of CO991132 was planted in Colorado to allow release of this line in autumn 2004, pending 2004 performance evaluations. As a backup, a smaller increase (five acres) of CO991132 was also planted in Yuma, Arizona. In addition to tests in Colorado, CO991132 was entered for regional testing in the 2004 SRPN and is again being grown along with CO00D007 in Westbred and AGSECO trials in Kansas and Montana.

Samples of all lines on foundation seed increase are being tested for milling and baking quality in our own quality laboratory, the USDA Hard Winter Wheat Quality Laboratory (Manhattan, KS), and various private industry collaborators. The *Clearfield*TM lines also were planted in replicated *Clearfield* Qualification Trials in autumn 2003, with five locations in Colorado and two locations in both Oklahoma and Nebraska with our counterparts in those states. As

we did not conduct the *Clearfield*TM qualification trials in 2003, we are hopeful that we will obtain the required data to support cultivar release in 2004.

The trials in 2003 were a drastic improvement over those in 2002. Yield averages ranged from 18.7 bu/acre at Walsh to 90.4 bu/acre at Akron, with a range of different yield levels in between. Although random, nongenetic variability at four locations (Lamar, Sheridan Lake, Genoa, and Bennett) prevented reliable data interpretation from those locations, data from the other six locations were sound and of great value for variety selection and recommendation. Based on agronomic, performance, pest resistance, and end-use quality evaluations, 16 experimental lines were retained and advanced for further testing. Small-scale seed increases of each of the lines retained for further testing were planted in autumn 2003. Seed supply from any of these lines that perform well in 2004 should be adequate to enable Breeder Seed increase in 2004–05 (for earliest possible release autumn 2006). In addition to continued yield testing, extensive milling and baking quality evaluations will be done on these materials during winter 2003–04 in the CSU Wheat Quality Lab, the USDA–ARS Hard Winter Wheat Quality Lab (Manhattan, KS), and by various private-industry collaborators. The Irrigated Variety Trial (IVPT) was planted at three locations in Colorado. Excellent separation among entries was observed at all locations, although marginal stands (due to late planting) and stripe rust adversely affected the Ovid trial location. A few HWW experimental lines performed quite well in the trials, especially CO99W254, which was at or near the top of the trial at all three locations. Although the baking quality of CO99W254 is in question, it is encouraging that we are beginning to identify experimental lines with very high yield potential for irrigated production conditions. Under these conditions, stripe rust may continue to be a concern and so we have begun to focus a bit more on stripe resistance in the crossing program. Good sources of resistance are available in Great Plains germ plasm and these sources should prove useful in the absence of a race change that makes them ineffective.

New Russian wheat aphid biotype. In late March through May 2003, reports were received of severe RWA infestations and plant damage in fields of Prairie Red winter wheat in southeastern Colorado. Infested plants in these fields displayed characteristic susceptible symptoms, raising concern that a new RWA biotype was present. Greenhouse seedling screening experiments with a colony reared from this isolate (provisionally denoted as biotype B) confirmed that it is virulent to all resistant wheat cultivars available in the U.S. hard winter wheat region, including the *Dn4*-based resistance deployed in several cultivars by CSU and the resistance from PI 220350 deployed by Kansas State University in the cultivar Stanton.

Upon confirmation of the presence of the new biotype, we evaluated a broad collection of resistance sources used in our breeding program. These sources included all previously numbered genes (*Dn1* through *Dn9*) in addition to eight other sources that have not received numbers but had shown promise in evaluations at CSU and elsewhere. With one exception, each of these sources proved to be as susceptible to the new biotype as the *Dn4* sources and Stanton. The lone exception, accession 94M370 from South Africa, showed a very high level of resistance to the new biotype. Unfortunately, the resistance in 94M370 is conferred by the *Dn7* gene that resides on a T1BL·1RS wheat–rye translocation has been associated with serious adverse effects on bread baking quality. We obtained a group of five lines from the USDA–ARS in Stillwater that carry this resistance and we are currently evaluating these in the field for their release potential.

In separate screening experiments, we also have identified effective resistance from two other sources. The first of these is an experimental line from the USDA–ARS in Stillwater, OK, designated 2414-11 (derived from PI 366515). The resistance in this source is currently being backcrossed into several elite backgrounds. The second resistance source is a group of lines from our own program that carry resistance from triticale accession PI 386148. The resistance in these triticale-based lines had previously been transferred to a Lamar background, yet we are presently uncertain about the stability of this resistance.

In an attempt to identify additional resistance sources, we recently completed the first evaluation of a collection of 761 wheat accessions from the National Plant Germplasm System. The accessions that we chose to evaluate showed a similar level of resistance to the original RWA biotype as the resistant cultivar Halt in systematic germ plasm evaluations conducted by the USDA–ARS in Stillwater, OK, in the 1990s. From the group of 761 accessions, we have identified a group of 68 accessions that show promise for a replicated follow-up evaluation planned for spring 2004. Only eight of these accessions, however, showed a level of resistance similar to the resistant check 94M370. Four of these are from Afghanistan (PI 135064, PI 366566, PI 366572, and PI 366589), two are from Iran (PI 140204 and PI 429398), one is from Kazakhstan (PI 572652), and one is from Tajikistan (CI 2401). Initial crosses have now been made with each of these resistance sources.

With very few resistance sources currently available, additional germ plasm screening is needed. We recently began the evaluation of a group of 7,000 Iranian landrace selections that are relatively new additions to the National Plant Germplasm System. These accessions have been evaluated by other researchers (e.g., CIMMYT, University of California–Davis) for RWA and other agronomic characteristics but have not been evaluated for resistance to the new RWA biotype present in Colorado. As many of the resistant accessions from the original screenings by the USDA–ARS originated from Iran, we expect that this collection will contain at least some resistant accessions.

Our resistance breeding strategy will emphasize the most rapid deployment of resistance possible in a new cultivar. An overriding objective of this effort will be the maintenance of a broad diversity of resistance sources to hopefully be better prepared in the event that additional biotypes are identified.

Graduate student research.

Several graduate student research projects are currently underway or were completed in 2002–03. Briefly, these projects include the following important areas of research: assessment of the breeding potential of gibberellic acid-sensitive semidwarfing genes that do not reduce coleoptile length (Sally Clayshulte); development of GIS technology to improve cultivar recommendations and identify cultivar-specific production and quality zones (Federico Pardina-Malbrán); identification of RWA biotype-B resistance sources and characterization of field protection provided by the *Dn7* RWA-resistance gene (Meghan Collins); and characterization (inheritance, allelism, and marker-tagging) of biotype B RWA resistance sources (Joshua Butler).

USDA–IFAFS Project.

We continue to work on backcrossing novel genes into our germplasm base through the multi-institutional grant effort funded by the USDA–IFAFS grant-funding agency. The focus of this grant, entitled Bringing Genomics to the Wheat Fields, is to utilize DNA marker technology as a means to transfer desirable quality and pest resistance traits into released cultivars and elite experimental lines. Our program at CSU is one of 12 public plant-breeding programs involved in this effort, with Dr. Nora Lapitan serving as co-investigator in our effort at CSU. When the program began 2 years ago, we chose recently released cultivars or advanced experimental lines (e.g., Avalanche, Above, Ankor, CO970547, Stanton, and Lakin) as target parents to transfer or combine genes for WSMV and BYDV tolerance (from wheatgrass), high grain protein content (from wild durum wheats), and RWA resistance. We have completed three cycles of MAS and are nearing the stage when improved populations will be grown in the field. Because of the identification of the new RWA biotype, we abandoned our efforts on transfer of the *Dn2* and *Dn4* resistance genes to different backgrounds. As a replacement for this project, we have begun the marker-based transfer of the *Yr5* and *Yr15* stripe rust-resistance genes into multiple backgrounds. Continued funding for this project past 2005 will depend on the success of a grant initiative to develop a national effort in MAS in wheat. Coordination of this effort is again through the University of California–Davis.

Germ plasm introduction.

In 2002–03, we continued our long-term effort to systematically explore wheat germ plasm from CIMMYT–Mexico and eastern European countries. The objective of this effort is to broaden the genetic diversity in our program in order to insure long-term genetic improvement primarily for yield under irrigated conditions and for stress tolerance under dryland conditions. Our strategy for using these sources is to evaluate them under field conditions in Colorado and then select among the larger group for the most promising sources for introgression. The crossing strategy that we are currently using is what we would call a ‘focused backcrossing’ approach where two or three backcrosses are made with one or two of our elite backgrounds and segregating progenies are identified in field nurseries. We are hopeful that we will identify recombinants that maintain the desirable characteristics of our recurrent parents while transferring in desirable genes from the wheat germ plasm sources.

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GEORGIA / FLORIDA

GEORGIA EXPERIMENT STATION / UNIVERSITY OF GEORGIA Griffin, GA 30223-1197, USA.

J.W. Johnson, R.D. Barnett, B.M. Cunfer, and G.D. Buntin.

The 2003 Georgia winter wheat crop was grown on about 380,000 planted acres, 9 % more than last year. Oat acreage was 100,000 acres, 18 more than last year. Acres planted to rye, 270,000, were 8 % less than last year. The crop production for wheat resulted in a state average yield of 50 bu/acre. The autumn planting conditions were very wet, which delayed small grain planting. Most of the planting was delayed by at least 2 weeks past optimum. Overall, the season was characterized by a mild and wet winter conditions followed by a wet and mild spring. Wet conditions prevailed through the harvesting stage, which resulted in low test weight, severe sprout damage, and high incidence of Fusarium for 75 % of the crop. The average rainfall during the small grain growing season was 33 % more than normal.

Breeding.

Wheat. **USG 3592** is a new cultivar developed by the University of Georgia and the University of Florida. The cultivar is derived from a single cross: Coker 9134/GA881502 (WM6525/GA821264//GA801468) and tested as GA 931241E16. USG 3592 is a medium-maturing, white-chaffed, medium-tall line that matures, on average, 2 days later than AGS 2000 in Georgia. The cultivar is resistant to currently predominant races of leaf rust and biotypes of Hessian fly in Georgia, moderately resistant to races of powdery mildew, and resistant to soilborne mosaic virus.

Oat. **Horizon 314** is a new, full-season winter oat variety coöperatively released by the Florida and Georgia Agricultural Experiment Stations in 1999. Well suited as a winter grazing crop for beef or dairy producers, Horizon 314 will make an excellent grain, hay, or silage crop and is excellent for wildlife plots. In comparison to Chapman, Horizon 314 is higher yielding, has a heavier test weight, is 3–6 days later in heading, and 4 inches taller in height. Horizon 314 has good winter hardiness, good crown rust resistance, tillers well, and has a dark green plant color. Horizon 314 was tested experimentally as FL92OHR31,314 and as FLX499-1-B3-G6. The cultivar was selected from material donated by the Northrup-King Seed Company (Novartis Seeds) to the USDA–ARS when the Coker Pedigreed Seed Company oat-breeding program (owned by Northrup-King) was discontinued in 1989. A large number (25,000) of single-panicle selections that had been harvested from the 1988 nurseries of the Coker program were planted at Quincy, FL, for evaluation in 1992. Horizon 314 was a single row, designated 31,314, selected from that material and originated from the cross (X499) 'Coker 84-15/TX84AB2171'.

Triticale. **Trical 342** is a new early maturing triticale cultivar for feed grain and silage production in the southeast U.S. Trical 342 was tested as FL91142-A19, which resulted from a cross made in 1991 at the North Florida Research and Education Center at Quincy, FL. The pedigree is 'Sunland/LAD 388'. LAD 388 is a winter triticale from Poland.

Across three locations, Trical 342 averaged 5,069 lbs of grain/acre compared to several checks in the trial; AGS 2000 wheat, 4,558 lbs/acre; Florico, 4,263 lbs/acre; Arcia, 3,393 lbs/acre; and Sunland, 3,296 lbs/acre.

Entomology.

Stand reductions of double-cropped cotton following canola (*Brassica napus* L.) as compared to winter wheat have been observed in the coastal plain region of the southeastern United States. This investigation was conducted to evaluate these observed stand losses and to examine the role of tillage, planting time, and pesticide use on stand establishment of double-cropped cotton following winter wheat and canola. One field study conducted near Plains, GA, in 2 years examined the effect of at-planting insecticide, aldicarb (Temik), and in-furrow fungicide treatment, quitozene plus metalaxyl (Terrachlor plus Ridomil Gold EC), on cotton stand establishment, disease and insect incidence, and yield when double cropped. Winter crop treatments were canola, wheat, or fallow. A second study conducted near Plains and Tifton, GA, in 2 years examined in a strip split-plot design the effect of tillage (conventional verses strip-tillage) and planting time (immediately after winter-crop harvest or 10 days later) on double-cropped cotton.

In all trials in 1999, cotton stand and seed cotton yields were reduced following canola as compared with wheat and/or fallow. Seedling insect populations were affected by winter crop but were not the cause of significant cotton stand loss. In four of five comparisons, cotton seedling infection by *R. solani* was greater following canola than winter wheat or fallow. All *R. solani* isolates were anastomosis group AG-4, indicating that canola production did not selectively increase an unusual biotype of *R. solani*. In both years, *R. solani* AG-4 infection rates were enhanced by use of aldicarb granular insecticide regardless of the preceding winter crop. The fungicide treatment did not prevent seeding infection by *R. solani* but did reduce stand and yield losses in 1999. Tillage had no consistent affect on *R. solani* AG-4 infection, stand, or yield following any winter crop treatment. Delayed cotton planting also did not consistently affect *R. solani* AG-4 infection and stand loss, but reduced yield at Tifton. Thus, modified tillage practices and delayed cotton planting are not viable management tools for controlling *R. solani* AG-4 infection and minimizing stand losses of cotton when double cropped following canola. No significant problems occurred with double-cropped cotton planted following winter wheat.

Pathology.

The two most widespread and damaging diseases in Georgia and the Southeast in 2003 were caused by stripe rust and wheat soilborne mosaic virus. The largest outbreak of stripe rust ever recorded from Texas to the northern Great Plains occurred in 2003. Predominated sources of resistance to stripe rust were from cultivars and lines with *Yr17* and *Yr18*. *Yr9* was affected in combination with *Yr18*. Cold, early-season temperatures also favored SBWMV. Plants were stunted by late winter and had leaves with a yellow mottled appearance. Several cultivars and lines were identified with resistance to SBWMV (Crawford, GA931241E16, PIO 26R61, USG 3209). Two new experimental lines (GA951079-2E31, GA951395-2E19) were resistant to both diseases.

Powdery mildew adult plant resistance. The cultivar Knox 62 is known to have adult-plant resistance to powdery mildew, but the relationship between the genes conferring its resistance and corresponding chromosomes has not been documented. To determine the chromosomal locations of adult-plant resistance genes, Knox 62 was crossed with the susceptible disomic Chinese Spring and a full set of Chinese Spring monosomic lines. The adult plants of F_2 populations and their parents were evaluated for resistance to powdery mildew in a condition of polycyclic infection, based on their infection type (IT), infected leaf area (ILA), area under disease development curve (AUDPC), and daily disease increase index (DDII) controlled in the glasshouse. Results indicated that the resistance genes in Knox 62 are mainly additive, and seven chromosomes were involved in the adult-plant resistance of this cultivar. Chromosomes 5A, 7A, 4B, and 5D carry genes showing positive effects on resistance, whereas chromosomes 3A, 1B, and 1D have factors increasing susceptibility. The segregation of the disomic F_2 populations and noncritical crosses fit a four-gene model, suggesting that chromosomes 5A, 7A, 4B, and 5D each contain one gene or one cluster of tightly-linked genes. The interactions between resistance genes and susceptibility genes seem to be in a complex epistatic manner.

Effect of rye chromatin in soft wheat. The effect of introgression of rye chromatin arm from the absence of a corresponding wheat chromatin arm has not been fully studied. The agronomic and milling and baking quality effects of the individual wheat and rye chromosome 1 arms in translocations, substitutions, and nontranslocation lines were deter-

mined. Chromosome arm 1RS significantly increased grain yield that was depended upon the source of rye chromatin. All translocations and substitutions involved with 1RL had a negative effect on agronomic performance and had significantly higher protein content. The 1RS translocations increased alkaline water retention capacity. The baking quality did not depend on the 1RS source in wheat-rye translocations but was depended upon the wheat chromatin, which was replaced by the rye chromatin. The 1RS translocations can be used to improve grain yield when the source is carefully selected from different wheat genetic background. The translocation T1RS·1BL gave the optimum for agronomic performance, whereas the T1RS·1AL was the best for milling and baking quality.

Effect of the T1D·1RS translocation. The influence of the T1DL·1RS genotype on agronomic performance and end-use quality was determined in two crosses. Grain yield and test weight of the Kanto/Gabo (T1DL·1RS) were significantly lower than nonsiblings, but no significant differences were observed in the other cross (Jaypee/Gabo). The effect of the translocation for quality traits were undesirable for cookie quality. The effects of the translocation on agronomic performance were modified by wheat genetic background, whereas milling and baking qualities were less affected.

Waxy wheat. The effect of starch amylose concentration on pasting properties and milling and baking quality was studied in eight granule-bound starch synthase (GBSS: waxy protein) genotypes in a soft wheat background. Double null lines showed lower amylose concentration than single null lines and wild-type lines. Milling and baking quality traits were clearly different between waxy (nil amylose) and the other genotypes. Waxy lines showed the lowest flour yield of 69.5 %. The typical A-type patterns of x-ray diffractograms were observed for all starches. No intensity peak at $2\theta = 23^\circ$ was observed for waxy starch. Waxy starch showed higher crystallinity than nonwaxy starch. Analysis by rapid viscoanalyzer showed distinctive differences among the eight genotypes. The peak viscosities of waxy starches were higher than those of all other genotypes. Breakdown and setback also differed.

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IDAHO**UNIVERSITY OF IDAHO****Moscow and Aberdeen, ID USA.**

R. Zemetra, E. Souza, S. Guy, B. Brown, N. Bosque-Pérez, J. Hansen, K. O'Brien, M. Guttieri, D. Schotzko, T. Koehler, L. Sorensen, J. Clayton, E. Jimenez, M. Rehman, and M. Kumar.

Production.

The 2003 Idaho winter wheat production was 57.6 million bushels, a 5 % increase from 2002. Acreage planted and harvested increased compared to 2002 and yield was similar for the 2 years. Moisture again was limiting in some areas in the late spring/summer resulting in lower test weight although there was a greater affect on spring wheat than winter wheat due to average to slightly above average precipitation in the winter and early spring. Stripe rust was again a problem though infection occurred late in moderately resistant cultivars and had minimal affect on yield. Statistics for the Idaho winter wheat production for the last 5 years are shown in Table 1.

Table 1. Statistics for Idaho winter wheat production for the last 5 years.				
Year	Acres planted (x 10 ³)	Acres harvested (x 10 ³)	Yield (bu/acre)	Production (bu x 10 ³)
1999	760	710	76	53,960
2000	780	730	90	65,700
2001	760	710	73	51,830
2002	730	690	79	54,510
2003	760	720	80	57,600

Personnel: Faculty.

Phi Berger, University of Idaho Plant Virologist based on the Moscow campus resigned to take a position as national program leader, biotechnology in APHIS. Robert Forster, University of Idaho Cereal Plant Pathologist at the Kimberly Research and Extension Center retired. Larry Robertson, University of Idaho Extension Cereals Specialist at the Aberdeen Research and Extension Center retired. Maury Wiese, University of Idaho Cereal Plant Pathologist based on the Moscow campus retired.

Roger Veseth, Conservation Tillage Specialist for the University of Idaho and Washington State University died 9 September, 2003, from complications after a sledding accident in March of 2003. Roger was 51 and had been working for the two universities since 1987. He promoted conservation farming technology in the region and was a key extension educator in the direct seed movement. Roger developed the PNW Conservation Tillage Handbook and coauthored the book Wheat Health Management with R. James Cook in 1991. Roger is survived by his wife, Clair, and four children.

Personnel: Graduate students.

Edgardo Jimenez completed his Ph.D. research on the effect of transgenic resistance to wheat viruses on plant-vector-virus relationships, and Karla Medina-Ortega joined the wheat entomology team to pursue an M.S. working on aphid vectors of BYDV. Sandy Castle completed her M.S. research on the effect of tillage practices on Hessian fly and its parasites. Maqsood Rehman completed his M.S. research concerning the potential for gene flow between wheat and jointed goatgrass and started his Ph.D. program investigating the affect of genome placement on gene migration of a transgene from wheat to jointed goatgrass.

Cultivar Development.

Moscow. The SWWW cultivar **Simon** was released by the SWWW-breeding program. Simon was tested in the Western Regional White Winter Wheat Nursery as 91-34302A. Simon is adapted to intermediate to high rain-fed areas and performs well under irrigation. Simon is the first winter wheat release from Idaho to carry the *Pchl* gene for *Pseudocercospora* footrot resistance.

The SWWW line **91-20503A** is being considered for release in 2004. 91-20203A is an early, short, semi-dwarf wheat with excellent yield potential under both rain-fed and irrigated conditions. The end-use quality of 91-20503A is good to excellent. The proposed name of 91-20503A is 'Dune'.

Aberdeen. The SWWW **Idaho 587** was released, which carries tolerance to the imidazolinone herbicides. Idaho 587 is nearly identical to Stephens in all other characteristics. Due to BASF's constraints of stewardship and PVP enforcement, seed partners McKay Seed, GMG LLC, Columbia Seed, McGregor Seed, and General Mills were selected to market Idaho 587.

The breeding line **IDO566** is proposed for release under the name Jerome. Jerome is derived from a cross to Westbred 926 and has greater grain yield than Westbred 926 and Westbred 936. Jerome has a yield potential similar to that of Jefferson in low-yield, rain-fed production and will likely be recommended as a complement to Jefferson and a replacement to Westbred 926 in northern Idaho and Westbred 936 in southern Idaho. Milling and baking quality of Jerome is similar to those of Westbred 936 and Jefferson. Jerome is the result of collaborative research with Nilsa Bosque-Perez, who identified its Hessian fly resistance.

Breeder seed increase has started for **IDO575**, a HRWW for low rainfall zones of southeastern Idaho. ISO575 has averaged approximately 2 bu/acre greater yield than Bonneville and Weston and is 2 inches taller than either wheat with less lodging. IDO575 has good emergence and end-use quality and is a candidate for release in 2005. Another line under consideration for release in 2004 is **IDO597**, a HWSW for irrigation and rain-fed production to replace Lolo and Idaho 377s. IDO597 has shown promise as a domestic wheat for bread and tortilla applications based on evaluations by domestic millers. Seed increase began in 2003 of IDO593 and will continue in 2004 with seed production. IDO593 is high yielding with good lodging resistance. The line also has exceptionally strong farinograph tolerance, similar to that of Klasic. Both IDO597 and IDO593 will be placed in extension testing in 2004 this year and be submitted to the Pacific Northwest Quality Council for evaluation in January 2005.

Entomology.

Edgardo Jimenez's dissertation research demonstrated for the first time that transgenic virus resistance in wheat can indirectly influence the life history and behavior of the bird cherry-oat aphid, *R. padi*. Sandra Castle's thesis research confirmed that eight species of Hessian fly parasites occur in Idaho. Parasitism levels vary widely depending on location and year, and range from 10 to 85 %.

Wheat molecular biology.

In the wheat straw lignin reduction project, three copies of the CCR1 gene in the lignin biosynthesis pathway have been isolated and sequenced from the cultivar Hubbard. An antisense form of CCR1 has been introduced into spring and winter wheat cultivars using particle bombardment in an attempt to lower the percent lignin in wheat straw.

Biological risk assessment.

Collaborative research on the potential for gene migration between wheat and jointed goatgrass continues with C. Mallory-Smith and O. Riera-Lizarazu at Oregon State University. D-genome, chromatin retention in jointed goatgrass backcross progeny was demonstrated to occur at expected Mendelian frequencies using molecular markers, indicating that genes on the shared D genome could be transferred between the two species if backcrossing is allowed to occur in the field. Work is currently underway to determine the affect of gene placement on the unshared A and B genomes of

wheat on gene migration and retention in jointed goatgrass backcrosses. A study of 'wheat/jointed goatgrass' hybrid phenotypes demonstrated that the phenotype of the hybrids was similar regardless of the wheat cultivar parent unless the parent was a club wheat. In the case of club wheat as a hybrid parent, the hybrid head was more similar to a common wheat head phenotype than the intermediate head type observed with common wheat crosses, making it difficult to identify hybrids between club wheat and jointed goatgrass in foundation seed fields.

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INDIANA**PURDUE UNIVERSITY**

**Departments of Agronomy, Entomology, and Botany and Plant Pathology, and the
USDA–ARS Crop Production and Pest Control Research Unit, Purdue University, West
Lafayette, IN 47907, USA.**

J.M. Anderson, S.E. Cambron, C.C. Collier, C. Crane, S.B. Goodwin, A. Johnson, J.A. Nemacheck, S. Scofield, B. Schemerhorn, R.H. Ratcliffe, R.H. Shukle, and C.E. Williams (USDA–ARS); H.W. Ohm, L. Kong, F.L. Patterson, H.C. Sharma, and J. Uphaus (Department of Agronomy); G. Buechley, D. Huber, G. Shaner, and J.R. Xu (Department of Botany and Plant Pathology); and J. Stuart (Department of Entomology).

Wheat production.

Indiana farmers harvested 174,089 hectares (430,000 acres) of wheat in 2003, up 30 % from 2002. According to the USDA National Agricultural Statistics Service, wheat yield in Indiana averaged 4,439 kg/ha (66 bu/acre) in 2003, up 25 % from the average yield in 2002. Little acreage was abandoned due to winter kill. Increasing interest in early maturing wheat cultivars in central and northern areas of Indiana is because of the continued profitability of double cropping; producing a crop of soybeans after wheat harvest in the same season.

New cultivars.

Three new SRWW licensed cultivars, **INW0301**, **INW0304**, and **INW0316**, were released and seed is being increased. INW0301, tested as P92226E2-5-3, has *H9* and *H13* for resistance to Hessian fly biotype L, *Lr37–Sr38–Yr17*, resistance to powdery mildew, leaf blotch, and soilborne mosaic virus, and has performed well in the midsouth U.S., likely due to its Hessian fly resistance. INW0304, tested as P97395B1-4-3-8, has moderate type-2 resistance to FHBt, resistance to glume blotch, leaf blotch, leaf rust, powdery mildew, SBWMV, and has *H13*. INW0316, tested as P961341A3-2-2, has resistance to yellow dwarf viruses from intermediate wheatgrass, *Th. intermedium*. All three cultivars are early, with heading dates similar to that of the cultivar Patterson.

Wheat disease summary.

Leaf and glume blotch were severe in the southern part of the state on susceptible cultivars. *Septoria tritici* persisted later into the season and blighted upper leaves more than in recent years, probably because of cool, wet weather during much of May. *Stagonospora nodorum* also was present and caused glume blotch. Stripe rust was evident as focal infections during May and early June but did not cause significant damage. Warm weather halted progress of the disease. Fusarium head blight was significant in southern Indiana this year, with up to 60 % infected spikes in some fields. In northern Indiana, up to 15 % of spikes were infected in many fields. Unusually cool weather throughout the state, especially at night during most of the grain-filling period, likely delayed development and spread of the disease after infection. Temperatures were much warmer beginning about 20 June, which was about 1 week prior to physiological maturity, and the disease began to spread significantly in infected spikes. The fungus did not develop during much of the grain-filling period because of cool temperatures, which allowed kernels to develop normally, and visibly scabby kernels were not conspicuous in harvested grain. However, fungal growth late in grain-filling produced significant toxin. Thus, levels of deoxynivalenol were higher than expected because kernels appeared fairly normal and grain quality was satisfactory.

Yellow dwarf viruses.

Resistance (Wiangjun, Ayala, Thompson, Balaji, and Anderson). The incorporation of intermediate wheatgrass - derived resistance gene(s) into improved wheat germ plasm generated a wheat substitution line, P29, which is completely resistant to cereal yellow dwarf virus (CYDV). The undetectable CYDV titer in P29 and related wheat lines led many to conclude that the resistance prevented viral replication. The purpose of this study is to test the hypothesis that *Th. intermedium*-derived resistance allows CYDV to replicate within the initially infected cells but inhibits viral movement. To determine whether CYDV replication or movement is inhibited, we examined the inoculated leaf for replication and uninoculated leaves for systemic spread. CYDV subgenomic RNA, produced only during replication, was found within the inoculated portion of the leaves of P29 and *Th. intermedium*, demonstrating that viral replication was not affected. The absence from the uninoculated, newly emerging leaves of inoculated P29 and *Th. intermedium* plants indicated the inhibition of viral systemic infection. Resistance could be overcome, resulting in a systemic spread of CYDV, if P29 was inoculated at the 1-leaf stage or younger with 50 to 100 viruliferous aphids/plant. As these infected P29 seedlings continued to grow, the resistance phenotype was recovered. However, when 7 to 10 aphids were used, the resistance was maintained across all developmental stages tested.

Our data suggest that *Th. intermedium*-derived resistance to CYDV was primarily dosage-dependent and could be developmentally regulated if the amount of inoculum was large enough. When testing for wheatgrass-derived resistance, the seedlings must be at least at the 2-leaf stage prior to inoculation with BYDV or CYDV. Based on our data, we propose three possible models for the mechanism of *Th. intermedium*-derived resistance to CYDV: 1) in the phloem-restriction model, once delivered into the plants, CYDV is restricted to the initially infected companion cells where it replicates, 2) in the inhibition of long-distance transport model, CYDV can spread from the infected companion cells into adjacent sieve elements but its movement beyond this point is blocked, or 3) in the inhibition of reentry model, CYDV can move systemically through sieve elements but cannot reenter the companion cells at distal locations for replication. The cellular localization of CYDV within the inoculated leaves of P29 is currently being investigated to test these models.

To increase the resolution of the RFLP-based map from *Th. intermedium*-wheat M4 recombinant lines (Crasta et al. 2000; Genome **43**:698-706), we added PCR-derived markers. To validate our mapping results, several M4 recombinant lines were analyzed by GISH and repetitive FISH DNA probes. Two M4 lines also were crossed with wheat and the F₂ progeny were examined for the presence of *Th. intermedium* segregating fragments. From this data we identified several diagnostic markers that conclusively identify field selections derived from *Th. intermedium*-containing material. This increased resolution also showed that, in most of the recombinant lines tested, the chromosome T7D·7E appeared as a mosaic of wheat and *Th. intermedium* chromatin sections. These lines are being examined in more detail to more fully understand the mosaic nature of these chromosomes.

Genetics and germ plasm (Sharma, Shen, Kong, and Ohm). We have research in progress to shorten the 7E chromosome segments in P961341 and KS24-2-11. P961341 is a Purdue line that has YDV resistance from intermediate wheatgrass and has the distal approximately three-fourths of the long arm of chromosome 7E from *Th. intermedium*. The YDV resistance is subtelomeric on 7EL. KS24-2-11 is a translocation line provided to us by K. Armstrong (Armstrong et al. 1993; Theor Appl Genet **85**:561-567) that has FHB resistance from tall wheatgrass (*Lophopyrum ponticum*). The FHB resistance is proximal to the centromere on the long arm of chromosome 7E12. We are characterizing segregating populations from a cross of 'P961341/CS *Ph1*' deletion line and segregating populations from a cross 'KS24-2-11/CS *Ph1*' deletion line.

We also are characterizing and genotyping segregating populations from a cross 'K11463/K2620'. K11463 and K2620 are substitution lines (Armstrong et al. 1993; Theor Appl Genet **85**:561-567). K11463 has chromosome 7E11 and is susceptible to FHB. K2620 has chromosome 7E12 and has resistance to FHB. Our objective is to achieve recombination between 7E11 and 7E12 to identify marker loci along the two chromosomes.

Septoria tritici blotch.

Mapping (Goodwin lab). Mapping of five genes for resistance to *Septoria tritici* blotch in wheat was completed last year. Work is now in progress to map QTL for resistance to this disease in a collaborative project with Dr. Hugh

Wallwork in Australia and to backcross the five previously identified single genes into a common susceptible background to use as differential cultivars.

We also are exploring quantitative RT-PCR for identification of resistant and susceptible lines of wheat to *Septoria tritici* blotch. Two approaches are being pursued 1) to measure fungal biomass and 2) to quantify gene expression in the host. Analysis of resistant and susceptible wheat plants from 1–27 days after inoculation showed that fungal biomass remained low in both resistant and susceptible plants until 12–14 days after inoculation. At this time, the fungal biomass increased rapidly in susceptible plants but remained near zero in the resistant plants. This may provide an accurate method of separating resistant and susceptible plants before symptoms are expressed fully.

To identify resistant plants even sooner, we are looking at the expression of 30 host genes during a time course and intensively at 12 hours after inoculation. Preliminary results indicate large differences between resistant and susceptible plants for the levels of gene expression, with a much higher expression in resistant plants compared to susceptible controls depending on the specific gene analyzed. Our goal is to identify resistant and susceptible plants at 12 hours after inoculation, without having to wait for 18 or more days for symptoms to be expressed. A rapid PCR test could greatly increase the throughput and efficiency of our resistance screening efforts compared to the usual greenhouse tests. However, it may be necessary to tailor the technique for each specific resistance gene analyzed.

Fusarium head blight.

Chemical control (Shaner and Buechley). Fungicides were evaluated for efficacy against FHB. Corn residue was the source of inoculum; mist irrigation promoted inoculum production and infection by *G. zeae*. Fungicides were applied at Feekes GS 10, 10.5, 10.51, or 10.52. All fungicide treatments, even those applied at GS 10, reduced incidence of head blight. Only the JAU6476 and V-10116 treatments applied during flowering reduced blight severity (the percentage of the head blighted on those heads that showed any blight). Most treatments reduced the number of *Fusarium*-damaged kernels. Several treatments applied at flowering reduced the DON level in grain. Three treatments increased yield significantly.

Epidemiology (Shaner and Buechley). We compared the effect of three densities of corn residue on the soil surface on abundance of *G. zeae* inoculum and FHB development. Early in the season, more spores of *G. zeae* were captured with Burkard volumetric samplers in plots with corn residue than in the plot with no residue. Later, no differences in spore capture among residue treatments were observed. Residue density had no effect on incidence or severity of FHB across three cultivars of different maturity that had each been planted at two dates. The general favorable weather for head blight largely obscured differences in local inoculum density.

Ratings in state wheat variety trials at four locations revealed differences among entries in incidence and severity of FHB. Correlations between *Fusarium*-damaged kernels and FHB index (an overall rating of head blight intensity, based on both incidence and severity) were low. Likewise, correlations between DON and FHB index or *Fusarium*-damaged kernels were low. None of these correlations had predictive value, meaning that grain quality, in terms of visible damage or DON, could not be predicted from head blight intensity, nor could DON content be predicted from amount of *Fusarium*-damaged kernels.

Germ plasm (Shaner and Buechley). We found a moderate but significant correlation between type-II and type-I resistance in repeated experiments ($r = 0.75$, $P = 0.0000$) among lines originally selected for type-II resistance. Between the two experiments, expression of type-II resistance was reasonably consistent ($r = 0.63$, $P = 0.0002$), but the expression of type I resistance was inconsistent ($r = -0.04$, $P = 0.83$). The poor correlation between expression of type-I resistance between the two experiments was largely the result of several lines that had a low severity in the first experiment but a high severity in the second experiment, which may have been related to use of different kinds of plastic bags used to cover heads for 48 h after inoculation.

For evaluation of type-I resistance, we sprayed heads with a suspension of conidia of *F. graminearum*. We compared two inoculum levels (2×10^4 versus 4×10^4 conidia/milliliter), two growth stages (GS 10.52 versus 10.54), and two patterns of inoculation (spray one side of head versus spray both sides). Cultivars with a range of resistance were used. Main effects of each factor were highly significant. A few interactions between cultivar and the other variables also were significant.

We evaluated type-II resistance in a population of RILs derived from a cross between wheat cultivars Chokwang (moderately resistant) and Clark (susceptible). The correlation between experiments for number of blighted spikelets 22 days after inoculation was 0.51. Transgressive segregation for greater resistance in Clark was greater than that shown by Chokwang.

Hessian fly.

Wheat Hessian fly interactions (Collier, Nemacheck, Puthoff, Sardesai, Subramanyam, Giovanini, and Williams). The expression of two closely related Hessian fly-responsive wheat genes, responding in incompatible interactions, were compared, using quantitative RT-PCR. One gene, *Wci-1*, was found to be a general stress-response gene that is up-regulated by aphids, virus infection, wounding, and various chemical elicitors of plant defense responses, in addition to the Hessian fly. *Hfr-1*, however, responded in a more specific way to Hessian fly and SA only. The up-regulation of *Hfr-1* was most dramatic in leaf sheath regions adjacent to larval feeding sites, although some systemic response was evident in leaf blades. These findings were confirmed in plant lines containing four different single Hessian fly-resistance genes infested with three different fly genotypes.

The wheat gene *Hfr-2* is up-regulated during compatible interactions, primarily near larval feeding sites. The expression of this gene increases dramatically in proportion to the level of larval infestation. The sequence of this gene appears to encode two domains, one similar to seed-storage proteins and the other similar to pore-forming proteins. This gene is not expressed in developing seeds, however. This gene may be partially responsible for the disruption of cell membrane integrity leading to leakage of water and nutrients for larval consumption.

Defense-response genes involved in hypersensitive response and oxidative burst appear to contribute little to wheat defense against the Hessian fly. Genes encoding several key enzymes such as NADPH oxidase, catalase, and superoxide dismutase do not respond to Hessian fly feeding. No response was visible when infested tissues were stained for the accumulation of peroxide with DAB (diaminobenzidine), an indication that the hypersensitive response is not active. Also, DPI (diphenylene iodonium), an inhibitor of the production of reactive oxygen species, did not allow the survival of avirulent larvae on treated resistant plants.

Avirulence genes (Stuart). Close linkage (3 ± 2 cM) was discovered between Hessian fly avirulence genes *vH3* and *vH5* on Hessian fly autosome 2 (A2). Bulk-segregant analysis discovered two DNA markers (28-178 and 23-201) within 10 cM of these loci and only 3 ± 2 cM apart. However, 28-178 was located in the middle of the short arm of Hessian fly chromosome A2, whereas 23-201 was located in the middle of the long arm of chromosome A2, suggesting the presence of severe recombination suppression over the proximal region of A2. To further test that possibility, an AFLP-based genetic map of the Hessian fly genome was constructed. Fluorescence in situ hybridization of 20 markers on the genetic map to the polytene chromosomes of the Hessian fly indicated there was good correspondence between the linkage groups and the four Hessian fly chromosomes. The physically anchored genetic map is the first of any gall midge species. The proximal region of mitotic chromosome A2 makes up 30 % of its length but corresponded to less than 3 % of the chromosome A2 genetic map.

Hessian fly populations (Alber, Johnson, Lu, Mittapalli, Schemerhorn, and Shukle). The historic record states there was a single introduction of Hessian fly into the United States. However, to date this hypothesis has not been tested. We are using mitochondrial genes and transposable element display (TE display) to reveal relationships within and between fly populations in the United and between these populations and populations in the Old World. Results are testing hypotheses concerning a single introduction into the U.S. and the presumed center of origin for the pest in the southern Caucasus of southwest Asia.

The salivary glands and midgut are of importance in the feeding of Hessian fly larvae on wheat. The role of salivary glands is being addressed by the ARS team at Manhattan, KS. We are cloning and characterizing midgut genes encoding enzymes involved in digestion. We hope to reveal basic information concerning digestive physiology in the pest and apply this knowledge to develop novel strategies toward achieving more durable resistance in wheat. We are using RNAi in experiments directed toward silencing/suppressing expression of midgut proteases in Hessian fly larvae and in testing compensation by the midgut proteases. Additionally, we hope to utilize WSMV to express the Bowman-Birk protease inhibitor in wheat and assess its effect on the development of Hessian fly larvae. If successful, this will establish WSMV as a transient expression vector to bioassay potential transgenes for Hessian fly resistance in wheat.

This coupled with knowledge emerging from the C. E. Williams laboratory identifying promoters for wheat genes up-regulated in the compatible interaction of Hessian fly larvae with wheat may allow site specific expression of transgenes for resistance in the plant, greatly facilitating the specificity and efficacy of transgenic resistance.

We have brought into culture two Hessian fly populations from Israel that display virulence to a wide range of resistance genes in wheat. From these populations we are selecting Hessian fly lines pure breeding for virulence to new resistance genes (e.g., *H31* and *H25*). These lines will be used by the Stuart laboratory at Purdue to develop mapping populations for fly genes controlling virulence to the resistance genes and by the Williams laboratory to reveal gene expression in wheat containing the resistance genes during compatible and incompatible interactions.

Research personnel.

William Bourdoncle, Ph.D. student with Herb Ohm, completed degree requirements and has accepted a corn breeding position with the Monsanto company in France. David Drake, Ph.D. student with Herb Ohm, completed degree requirements and is Extension Agronomist, Utah State University, Richfield, UT. Ousmane Boukar, Ph.D. student with Herb Ohm, completed degree requirements and is Scientific Director, IRAD Agriculture Research Station, Maroua, Cameroon.

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KANSAS

KANSAS AGRICULTURAL STATISTICS

Room 200, 632 S.W. van Buren, P.O. Box 3534, Topeka, KS 66601-3534, USA.

Jagger remains number one cultivar.

Jagger was the leading variety of wheat seeded in Kansas for the 2004 crop. Accounting for 40.9 percent of the state's wheat, Jagger decreased 4.3 points from a year ago but was the most popular cultivar in seven of the nine districts. The KSU-maintained cultivar 2137 ranked second, with 8.6 percent of the acreage, and ranked in the top 5 for all nine districts. TAM 110 remained in third

position, increasing nearly 1 point from last year. Trego, a hard white wheat, moved up to fourth place with 3.5 percent of the acreage. New to the top ten is Jagalene, ranking fifth with 3.0 percent. The OSU-maintained cultivar 2174 moved down to sixth place with 2.8 percent of the state's acreage. Karl and improved Karl fell to seventh place, with 2.3

Table 1. Top 10 wheat cultivars grown in the state of Kansas for the 2004 crop and percent of seeded acreage.

1. Jagger	40.9	6. 2174	2.8
2. 2137	8.6	7. Karl	2.3
3. TAM 110	4.2	8. Ike	2.0
4. Trego	3.5	9. T81	1.8
5. Jagalene	3.0	10. Dominator	1.5

percent. Ike held eighth place with 2.0 percent. New to the top ten is T81, ranking ninth with 1.8 percent. Dominator remained in the top ten with 1.5 percent. Acres planted with blended cultivars were not included in the rankings by cultivar. Blends accounted for 15.2 percent of the state's planted acres and were used more extensively in the north central and central areas of the state. Out of the total acres planted with blends, 92.4 percent included Jagger in the blend and 50.2 percent had 2137 in the blend. Hard white cultivars accounted for 4.9 percent of the state's acreage. Trego was the leading hard white cultivar, accounting for 72 percent of the state's white wheat. The majority of the white wheat was planted in the western third of the state. This wheat cultivar project is funded by the Kansas Wheat Commission.

Table 2. Distribution of Kansas winter wheat cultivars, 2004 crop (— = cultivar not reported in this district; 0 = < 1 %).

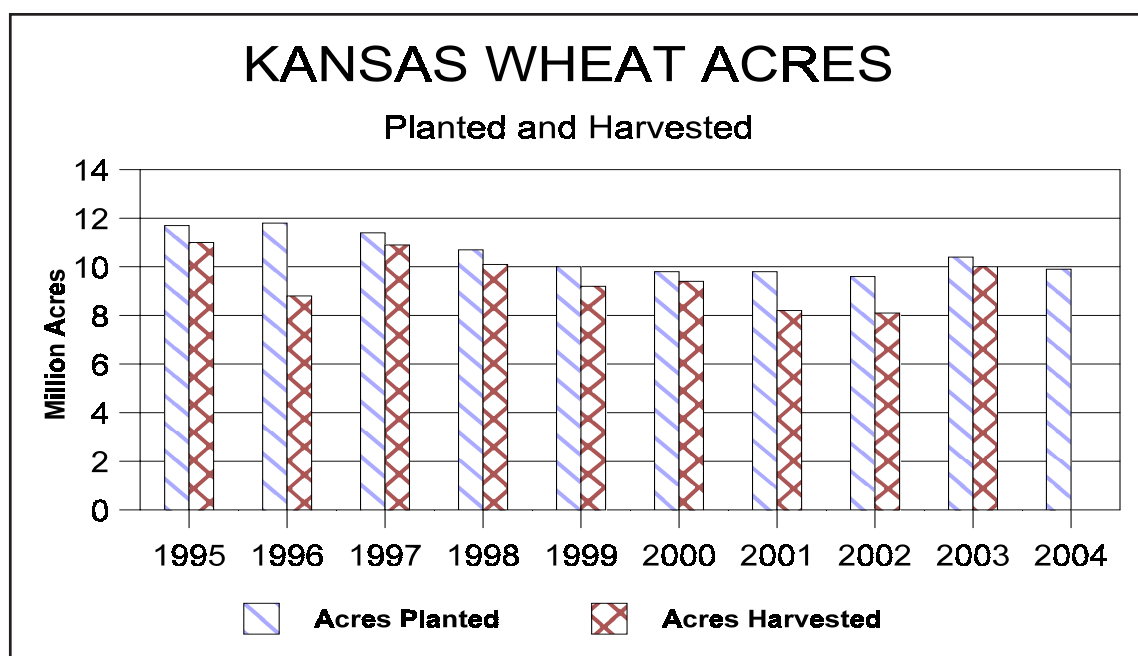
Cultivar	Agricultural Statistics Districts									State
	NW	WC	SW	NC	C	SC	NE	EC	SE	
	percent of seeded acreage									
Jagger	33.0	14.9	32.5	28.2	43.1	60.5	10.5	41.0	35.9	40.9
2137	9.1	8.5	8.2	8.0	12.1	6.5	19.5	26.5	21.9	8.6
TAM 110	0.5	16.5	13.7	—	0.1	0.3	—	—	—	4.2
Trego-HWWW	8.1	11.1	6.6	1.0	0.9	0.3	—	—	—	3.5
Jagalene	3.4	2.2	2.4	3.4	1.9	3.5	3.3	3.3	5.6	3.0
2174	—	0.1	0.1	0.3	2.9	6.2	1.4	1.5	13.7	2.8
Karl/Karl 92	1.8	0.9	0.4	8.5	2.2	1.2	19.7	7.2	1.3	2.3
Ike	1.0	4.4	7.6	0.2	1.5	0.1	—	—	—	2.0
T81	0.4	5.8	7.1	—	0.1	0.0	—	—	—	1.8
Dominator	0.1	0.1	—	5.1	4.7	0.5	4.9	4.0	0.1	1.5
2145	1.0	0.3	0.1	3.9	2.1	1.0	20.6	6.3	3.0	1.5
Stanton	3.5	5.7	1.9	0.3	0.1	—	—	—	—	1.4
Thunderbolt	6.2	1.8	1.5	0.6	1.1	0.2	—	—	—	1.4
TAM 107	3.0	3.0	3.7	0.0	0.1	0.3	—	—	—	1.3
Akron	0.5	6.9	—	—	0.0	—	—	—	0.1	0.9
Cutter	0.0	0.0	0.0	0.2	0.3	1.8	0.2	—	0.0	0.7
NuFrontier-HWWW	1.9	1.7	1.0	0.2	—	0.0	—	—	—	0.6
Coronado	—	0.0	—	0.1	0.1	1.5	0.0	0.5	0.1	0.5
TAM 105	—	3.2	0.1	—	—	—	—	—	—	0.4
Larned	0.4	0.9	1.4	0.1	0.0	0.1	—	0.1	—	0.4
2163	—	0.4	0.1	0.4	0.8	0.2	1.2	2.6	0.6	0.3
Lakin-HWWW	0.5	0.2	1.2	—	—	0.1	—	—	—	0.3
Ogallala	0.5	0.5	0.6	0.1	0.0	0.1	—	—	—	0.3
Vista	1.8	0.4	—	—	—	—	—	—	—	0.2
Above	0.6	0.9	0.1	0.1	0.0	0.0	—	—	—	0.2
Scout/Scout 66	—	0.1	1.2	0.1	0.0	0.0	—	—	—	0.2
Tomahawk	0.0	0.1	0.6	0.3	—	0.2	—	0.5	—	0.2
Venango	0.0	—	—	0.1	0.1	0.4	0.3	0.3	0.3	0.2
Alliance	1.7	—	—	—	—	—	—	—	—	0.2
Platte-HWWW	0.4	0.1	0.8	—	—	—	—	—	—	0.2
NuHorizon-HWWW	0.5	0.1	0.4	0.2	—	—	—	—	—	0.2
Blends	16.0	5.9	4.1	35.2	23.4	13.3	15.9	2.3	5.9	15.2
Other HWWW Cultivars	0.2	0.5	0.5	0.3	0.1	0.2	—	0.4	—	0.1
Other Hard Cultivars	3.9	2.8	2.1	3.1	2.5	1.5	2.5	3.5	8.9	2.5
Other Soft Cultivars	—	—	—	—	—	—	—	—	2.6	0.0
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

Table 3. Distribution of Kansas winter wheat cultivars, specified years.

	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004
Cultivar	percent of seeded acreage									
Jagger	—	1.0	6.4	20.2	29.2	34.0	35.8	42.8	45.2	40.9
2137	—	—	1.0	13.5	22.0	23.1	22.3	15.5	13.3	8.6
TAM 110	—	—	—	—	0.5	1.3	2.8	3.0	3.8	4.2
Trigo–HWWW	—	—	—	—	—	—	0.3	0.8	1.8	3.5
Jagalene	—	—	—	—	—	—	—	—	—	3.0
2174	—	—	—	—	—	1.1	3.0	3.1	3.1	2.8
Karl/Karl 92	22.4	20.9	22.1	10.8	5.9	3.5	3.3	3.6	3.2	2.3
Ike	0.9	7.2	10.5	7.0	5.5	4.1	3.6	2.6	2.1	2.0
T81	—	—	—	—	—	0.2	0.2	0.8	0.6	1.8
Dominator	—	—	—	0.2	0.8	1.4	1.5	2.0	2.2	1.5
2145	—	—	—	—	—	—	—	—	—	1.5
Stanton	—	—	—	—	—	—	—	0.1	0.6	1.4
Thunderbolt	—	—	—	—	—	—	0.2	0.6	0.8	1.4
TAM 107	20.6	17.1	17.0	12.6	8.3	6.3	5.3	2.9	2.3	1.3
Akron	—	—	—	0.4	0.8	1.0	0.4	0.4	0.2	0.9
Cutter	—	—	—	—	—	—	—	—	—	0.7
NuFrontier–HWWW	—	—	—	—	—	—	—	0.1	0.3	0.6
Coronado	—	—	—	0.8	1.3	1.0	1.1	0.7	0.8	0.5
TAM 105	—	—	—	—	0.3	0.4	0.1	—	—	0.4
Larned	7.6	4.8	3.6	2.4	1.9	1.2	1.0	0.9	0.8	0.4
2163	17.1	19.8	15.4	10.4	3.4	2.3	2.0	1.3	0.8	0.3
Lakin–HWWW	—	—	—	—	—	—	—	0.1	0.2	0.3
Ogalala	0.2	1.5	1.3	0.8	0.7	0.8	0.4	0.4	0.2	0.3
Vista	0.3	0.8	1.2	1.1	0.9	0.9	1.0	0.9	0.3	0.2
Above	—	—	—	—	—	—	—	—	—	0.2
Scout/Scout 66	1.0	1.2	0.8	0.7	0.5	0.3	0.1	0.2	0.2	0.2
Tomahawk	7.0	4.7	3.1	1.8	1.2	0.8	0.4	0.3	0.1	0.2
Vennago	—	—	—	—	—	—	—	0.1	0.1	0.2
Platte–HWWW	—	—	—	—	—	—	—	—	—	0.2
NuHorizon–HWWW	—	—	—	—	—	—	—	—	0.2	0.2
Blends	—	—	—	2.6	6.1	7.5	7.0	11.4	12.8	15.2
Other HWWW Cultivars	—	—	—	—	—	0.2	0.8	0.3	0.2	0.1
Other Hard Cultivars	15.5	12.7	10.3	9.0	7.0	4.7	3.8	8.3	3.0	2.5
Other Soft Cultivars	—	—	—	—	0.0	2.0	0.0	0.1	0.1	0.0
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

Table 4. Top wheat cultivars planted in Kansas by district and percent of seeded acreage in 2004.

DISTRICT 10 (NORTHWEST)		DISTRICT 40 (NORTH CENTRAL)		DISTRICT 70 (NORTHEAST)	
Jagger	33.0	Jagger	28.2	2145	20.6
2137	9.1	Karl/Karl 92	8.5	Karl/Karl 92	19.7
Trego-HWWW	8.1	2137	8.0	2137	19.5
Thunderbolt	6.2	Dominator	5.1	Jagger	10.5
Stanton	3.5	2145	3.9	Dominator	4.9
DISTRICT 20 (WEST CENTRAL)		DISTRICT 50 (CENTRAL)		DISTRICT 80 (EAST CENTRAL)	
TAM 110	16.5	Jagger	43.1	Jagger	41.0
Jagger	14.9	2137	12.0	2137	26.5
Trego-HWWW	11.1	Dominator	4.7	Karl/Karl 92	7.2
2137	8.5	2174	2.9	2145	6.3
Akron	6.9	Karl/Karl 92	2.2	Dominator	4.0
DISTRICT 30 (SOUTHWEST)		DISTRICT 60 (SOUTH CENTRAL)		DISTRICT 90 (SOUTHEAST)	
Jagger	32.5	Jagger	60.5	Jagger	35.9
TAM 110	13.7	2137	6.5	2137	21.9
2137	8.2	2174	6.2	2174	13.7
Ike	7.6	Jagalene	3.5	Jagalene	5.6
T81	7.1	Cutter	1.8	Onago	4.1



KANSAS STATE UNIVERSITY

**Environmental Physics Group, Department of Agronomy, Kansas State University,
Throckmorton Hall, Manhattan, KS 66506-5501, USA.**

Nitrogen mineralization rate of soil beneath a closed animal waste lagoon.

Fernando Madrid and M.B. Kirkham.

We reported in the *Annual Wheat Newsletter* of 2001 that wheat took up more nitrogen from soil at the bottom of a closed animal waste lagoon than it did from a Haynie very fine sandy soil, a common, nearby agricultural soil. The results showed that lagoon soil is a good fertilizer source and that the high levels of $\text{NH}_4\text{-N}$ in it are not toxic. We have continued the work with the lagoon soil, and here we report its rate of mineralization after closure. Soil was collected at three locations from a freshly emptied lagoon near Manhattan, KS: middle, southwest corner, and 18 m north of the southwest corner (same locations as reported in 2001). Soil samples were incubated for 0, 1, 2, 3, 4, 6, 8, 12, 20, or 30 weeks. Mineralization rate in the lagoon soils was compared to that of the Haynie soil. The soil from the middle of the lagoon had the highest initial concentration of $\text{NH}_4\text{-N}$ (882 mg/kg). By comparison, the Haynie soil had a concentration of 2.8 mg/kg $\text{NH}_4\text{-N}$. The conversion of the $\text{NH}_4\text{-N}$ to $\text{NO}_3\text{-N}$ in the soil from the middle of the lagoon was complete after 4 weeks, when the $\text{NH}_4\text{-N}$ concentration was 1.18 mg/kg and the $\text{NO}_3\text{-N}$ concentration was 1,094 mg/kg. During this 4-week period, $\text{NO}_3\text{-N}$ increased at a rate of 36.5 mg/kg per day. If all this $\text{NO}_3\text{-N}$ escaped to ground water, the U.S. drinking water standard for $\text{NO}_3\text{-N}$ (10 mg/l) would be exceeded by over three times. The results showed that $\text{NH}_4\text{-N}$ is converted rapidly to $\text{NO}_3\text{-N}$ (within a month) in the soil beneath a closed animal waste lagoon and that, once a lagoon becomes aerobic, the $\text{NO}_3\text{-N}$ formed would pose a serious threat to ground water.

News.

Dr. M. Stanley Liphadzi has returned to South Africa and now manages the Sustainable Rural Livelihoods program of the Grain and Industrial Crops section of the Agricultural Research Council. His address is: SRL Manager, Grain & Industrial Crops, Agricultural Research Council (ARC), Central Office, 1134 Park Street, Hatfield, Pretoria 001, South Africa.

Dr. J.K. (Ken) McCarron joined the group 1 March 2004 as a Visiting Scholar.

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THE WHEAT GENETICS RESOURCE CENTER**Department of Plant Pathology, Throckmorton Hall, Manhattan, KS 66506-5502, USA.****<http://www.ksu.edu/wgrc>**

B.S. Gill, W.J. Raupp, B. Friebe, L. Huang, V. Kuraparthi, W. Li, M. Pumphrey, L. Qi, D. See, D.L. Wilson, and P. Zhang.

Cytogenetic stocks.

New addition lines. Recently we reported on the development of a complete set of wheat–*Ae. speltoides* chromosome addition lines (Friebe et al. 2000). This set of addition lines is especially interesting because the S genome of *Ae. speltoides* is considered as the most closely related genome in the Sitopsis group to the B genome of *T. aestivum*. By crossing the addition lines with the appropriate B-genome monosomic stocks, we have produced six S(B) chromosome substitution lines. Once this set has been completed, these stocks will allow us to determine the sporophytic and gametophytic compensating ability of the S-genome chromosomes.

Previously, we reported that the short arm of the *E. trachycaulus* chromosome 1H¹ has a gene that confers resistance to leaf rust. We have produced a compensating wheat–*E. trachycaulus* Robertsonian translocation (T1H¹·1BL), in which the short arm of 1H¹ is translocated to the long arm of wheat chromosome 1B (Friebe et al. In press).

Genetics and genomic analysis.

Gc genes. Gametocidal (*Gc*) genes transferred from related *Aegilops* species into wheat cause chromosome breakage in the first postmeiotic interphase in gametophytes lacking them resulting in a preferential transmission of the *Gc*-carrier chromosome and semisterility. *Gc* genes may have played a significant role in karyotype evolution in the *Triticum/Aegilops* complex and were also used to produce a set of more than 400 deletion stock in wheat.

We have developed an efficient assay to identify knockout mutations at the *Gc2* locus that was transferred to wheat from *Ae. sharonensis* and is present in the T4BS·4BL·4S^{sh}L 'cuckoo' translocation chromosome. We mutagenized 5,000 hemizygous *Gc2*– seeds with EMS, and putative knockout mutations were identified by their restored spike fertility. Two *Gc2* mutants were obtained, verified by transmission studies and progeny screening, which mapped the mutation to the *Gc2*-carrier chromosome. The data show that no chromosome breakage occurs in the mutants, leading to a Mendelian segregation of the *Gc2*-carrier chromosome and restored fertility. The data support the dual function model of *Gc2* action, suggesting that this locus encodes for a 'breaking' and 'protecting' agent and that at least one of the two mutations is a knockout of the gene encoding for the 'breaking' agent (Friebe et al. 2003).

Rust resistance. We have cloned and were successful in transforming the leaf rust-resistance gene *Lr21* (Huang et al. 2003). We can now use a molecular approach for breeding wheat for durable rust resistance. Located at the distal end of chromosome 1DS, *Lr21* is located at a single locus. This gene is represented in *Ae. tauschii* by an allelic series. By examining the diversity of alleles, we hope to understand the response to selective pressure at the *Lr21* locus. We have sequenced 4,875 bp of DNA from each of the diploid alleles of *Lr21* to examine the entire coding regions, introns, and partial flanking sequences. A low level of polymorphism exists between resistant and susceptible alleles.

We searched for a new *Lr21* allele in the WGRC germ plasm collection. Twelve additional accessions of *Ae. tauschii* were identified that have an *Lr* gene at the *Lr21* locus. The geographical distribution of these *Lr21* alleles mainly is restricted along the area adjacent to the Caspian Sea in Iran and Azerbaijan. These accessions were collected within an 800-km distance of each other. All 12 accessions have an identical *Lr21* gene. In addition, the DNA sequences of the 442-bp region flanking the gene are identical.

We also studied the susceptible *lr21* allele in 13 accessions of *Ae. tauschii*. Five of the 13 accessions were collected from the same collection sites as the *Lr21*-carrying accessions. Three were collected along the Caspian Sea within 51 km of the *Lr21* accessions. The remaining five lines were collected in the places where no accessions with

Lr21 are found. Variations among the accessions lacking the gene, using *Lr21* as a standard, include 32 SNPs and 14 insertion or deletion polymorphism (Indels). About 44 % of the SNPs were detected in the LRR region, 22 % each in the N-terminal and 3'-nontranscribed regions (NTR), 9 % in the NBS region, and 3 % in the 5'-NTR. Large numbers of Indels were found among the accessions. Three of the Indels happened in either the nontranscript region (Indel 1) or an intron (Indel 4 and 5). All the remaining 11 Indels reside in the coding region, and eight of them may cause a frame shift, which results in a truncated protein.

The gene *Lr21* is a young allele that originated from an old locus. The birthplace of the resistance allele *Lr21* is in the area of Ramsar, Iran. All accessions collected from Ramsar have the same *Lr21* gene. This data suggests that a high leaf rust pressure existed in that area. This pressure helped to eliminate the old, susceptible *lr21* allele.

Identifying resistance gene analogs. Resistance-gene analogs (RGAs) have the potential to serve as closely lined markers for marker-assisted breeding or resistance-gene candidates. Eight new wheat RGAs and 26 kinase analogs (KAs) were isolated. Their clones detected fragments on all chromosomes except 4D (Maleki et al. 2003). Both simple and complex loci were identified indicating both single and multigene families. These RGAs and KAs will be useful as markers for mapping resistance gene loci in wheat.

Deletion stocks. We have characterized molecularly the core set of deletion stocks (Qi et al. 2003). One hundred fifty of the 159 deletion intervals or chromosome bins were tagged. Although most deletions were found to have a normal chromosome constitution, others may have arisen by translocation from unknown chromosomes. We discovered 35 new deletions in 26 of the lines. We also were able to detect aberrations in some genetic stocks. Any target gene can be allocated to a specific 28-Mb bin and associated ESTs and anchored to the other Triticeae and grass maps for molecular cloning by comparative and wheat-based positional cloning methods.

Altered gene expression in wheat. We are trying to understand how the three wheat genomes work within the nucleus by comparing gene expression in a synthetic hexaploid wheat with its diploid (*Ae. tauschii*) and tetraploid (*T. turgidum*) parents. We found that expression of a significant fraction of genes was diminished in the synthetic wheat but some were activated (He et al. 2003). Gene silencing appears to be caused by gene regulation and not due to chromosome or DNA loss.

Map-based cloning strategy in wheat. We have attempted the molecular cloning of three genes in wheat, *Ms3*, *Q*, and *Lr21*. *Ms3* is located in the proximal 40 % of 5AS, *Q* is at 87 % of 5AL, and *Lr21* is in the telomere, > 96 %, of 1DS. *Ms3* is in a gene-poor region with highly suppressed recombination and, therefore, is not a good candidate for map-based cloning. The *Q* region is relatively gene-rich, high in recombination, and a candidate gene has been identified. The *Lr21* region is highly gene-rich, extremely high in recombination, and the gene has been cloned and verified by transformation. What this means for wheat is that genes mapping in the proximal 50 % of the arms (especially the short arms) are not amenable to map-based cloning, those in the distal regions (> 0.5–0.90) can be cloned with difficulty, and those mapping in the telomeric regions (> 0.9) are easily accessible to map-based cloning.

Resistance to wheat curl mite. We have transferred resistance to the wheat curl mite from *Ae. tauschii* and rye to common wheat in the germ plasm line WGRC40. The rye-derived resistance gene is *Cmc3* and is present on the wheat-rye translocation chromosome T1AL-1RS. We have used the marker SCM09 to select for wheat lines carrying the 1RS segment and *Cmc3* (Malik et al. 2003). Two additional markers (GDM141 and KSUG8) flank the gene *Cmc4* on chromosome 6DS. These markers will be of use in wheat-breeding programs to select for lines with either of the two wheat curl mite-resistance genes.

Chromosome engineering of the *Wsm1* gene. *Wsm1*, specifying resistance to wheat streak mosaic virus (WSMV), is derived from *Agropyron intermedium*, where the complete arm of a group 4 *Ag. intermedium* chromosome is translocated to the long arm of wheat chromosome 4D, T4Ag-4DL (Friebe et al. 1994). *Wsm1* provides immunity against WSMV but negatively impacts yield. We have transferred the T4Ag-4DL translocation in a homozygous *ph1b/ph1b* background, where the 4AgS arm may pair and recombine with the homoeologous 4DS arm of wheat.

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GRAIN MARKETING AND PRODUCTION RESEARCH CENTER
U.S. Grain Marketing Research Laboratory, USDA, Agricultural Research Service,
Manhattan, KS 66502, USA.

O.K. Chung, G.L. Lookhart, F.E. Dowell, M. Tilley, S.R. Bean, L.M. Seitz, B.W. Seabourn, S.H. Park, J.L. Steele, M.E. Casada, M.S. Ram, E.B. Maghirang, M.C. Pasikatan, Y.S. Kim, D.B. Bechtel, J. Perez-Mendoza, F. Xie, R.K. Lyne, H. Singh, M.S. Caley, J.D. Wilson, D.L. Brabec, J.B. Ohm, J.E. Throne, J.E. Baker, T.C. Pearson, and Z.L. Haden.

Development of a micro-scale procedure to prepare wheat flour tortillas.

S. Arora, R. Lyne, J.N. Alviola, G.L. Lookhart, R.D. Waniska, and O.K. Chung.

Processing parameters for a microprocedure were established to produce wheat flour tortillas. Two laboratories were involved in optimizing a heated, hand-press (DP2000, Dough-Pro) and griddle parameters to produce tortillas comparable with those produced by pilot-scale Lawrence equipment. Press conditions of 55–105°C, 3–10 sec, and 5–12 kg, attached to the handle were evaluated. Griddle conditions of 150–250°C and 30–120 sec were evaluated. Tortillas were evaluated for opacity, diameter, thickness, shelf stability and textural properties. Fourteen flours were prepared into dough (42 g) and tortillas using both types of equipment. Good quality tortillas have large diameter, high opacity, and long shelf-stability. Processing parameters for the Dough-Pro and the griddle were established that yielded tortillas with properties similar to those made using pilot-scale equipment. Processing conditions of the Dough-Pro were 74°C, 7 sec, 12 kg, and ‘thin’ setting with the griddle at 160 +5°C for 80 sec. Under these conditions, tortilla diameter and opacity scores positively correlated to results from the Lawrence equipment. Similar trends were observed among the two laboratories. This microprocedure can be utilized when sample amount is limited, such as early-generation variety testing, and/or pilot-scale equipment is unavailable.

Comparison of different strip length for evaluating rheological properties of tortillas.

H. Singh, R.K. Lyne, O.K. Chung, P.A. Seib, and G.L. Lookhart.

Inherent variations during tortilla processing, and the product itself, have been major hurdles in objective measurements of rheological and textural properties. Tear and stress relaxation (SR) were measured using a texture analyzer (TAXT2 Plus) on the three-sized strips, including short, medium, and long (37, 60, and 75 mm, respectively) with 35-mm width. For the first set of experiments, six each of short, medium, and long strips were cut from the same tortilla, and it was replicated three times. For the 2nd set of experiments, 30 short, 20 medium, and 16 long strips were cut from each tortilla. In both sets of experiments, the maximum tear force decreased (approximately 32 %), the distance of rupture increased (approximately 74 %), and the area under the curve (absorbed energy) increased (58 %) by increasing strip length of 37 to 75 mm. The percent coefficient of variance (CV) values were 10 to 15 % by the strip length, 21 % for the area under the curve, and only 1 to 3 % for the %SR. The increase in %SR was from 52.88 and 52.70 to 66.81 and 67.26, respectively, for both sets of experiments, showing the consistency of the data within one tortilla and within a set of tortillas. However, %CV varied 10–27 % for the force required to stretch the tortilla to 1 mm during SR, likely due to the variation resulting from only one or two low data points from possible non-homogeneous weaker area of the tortillas. The conclusions were that (a) short (37-mm) strips were as reliable as medium (60-mm) or long (75-mm) strips for measuring rheological properties of tortillas; (b) they showed the same % changes, irrespective of the length of the length for both sets of experiments; and (c) the %SR values showed the smallest %CV values.

The staling of wheat flour tortillas studied by a texture analyzer and SE-HPLC.

H. Singh, R.K. Lyne, O.K. Chung, P.A. Seib, and G.L. Lookhart.

Staling has been a major cause of quality loss in tortillas but has been poorly understood at the molecular level. This research was a study of the changes involved in staling using a texture analyzer (TAXT2 Plus) and size-exclusion high-performance liquid chromatography (SE-HPLC). Tortillas were made in duplicate from wheat flour. The changes in stretchability and stress relaxation (SR) with storage time; 0, 1, 2, 4, 6 and 8 days; were studied using tortilla extensibility tests. The average of values plotted against time for these parameters showed a linear relationship up to 4 days of storage then reached a plateau. When the stretchability was followed from day 0 to day 8, the max force increased from 6.5 to 12 N and the modulus of deformation from 1.5 to 9.99 N/mm. Stress relaxation, a determinant of viscoelastic behavior, decreased by ~10 % during 8 days of storage. Another batch of tortillas from the same processing day were freeze dried after similar storage times, ground, and sieved (150 m), and used to follow changes in extractable protein (in 1-propanol, 50 %) using SE-HPLC. The decrease in polymeric void volume peak in SE-HPLC chromatogram with increase in storage time suggested the involvement of protein during staling of tortillas.

Polyphenol oxidase activity in wheat grain kernels, meals, and flours in relation to noodle color.

O.K. Chung, S.H. Park, and P.A. Seib.

Many studies revealed that darkening of noodles is related to the PPO activity. The PPO activity of whole wheat, meal, and flour was studied in relation to alkaline noodle color (L^*) after 24 hr. We tested 72 HRWW samples, including 46 from the Southern Central Plain (SCP) and 26 from the Wheat Quality Council (WQC) grown in 2002. Whole-kernel PPO was determined and milled wheat PPO by modifications of the method. The correlations (r , $n = 72$) between kernel and meal, kernel and flour, and meal and flour PPO levels were, respectively, 0.72, 0.48, and 0.47 ($P < 0.0001$). The PPO test reproducibility with meal had CV = 2.0 %, flour 9.8 %, and kernel 12.4 %. For the SCP set ($n = 46$), the PPO was negatively correlated with noodle color using kernels ($r = -0.57$), meal ($r = -0.67$), and flour ($r = -0.34$, $P < 0.05$), whereas the WQC set did not show significant correlations. Noodle color was correlated with flour protein content ($r = 0.74$) in the WQC set with a protein range of 10.4–14.7 %, but not in the SCP set with a protein range of 11.1–13.4 %.

Comparison of pup straight dough method with pound sponge and dough method and pup sponge and dough method.

M. S. Caley, O.K. Chung, S.H. Park, and Z.L. Haden.

Experimental test baking at Hard Winter Wheat Quality Lab of GMPRC has used the pup straight dough method (PSTD) since 1937 to investigate the potential of flour quality for white pan bread using early generation wheat progenies from breeders. This method may seem at odds with the commercial bread baking industry, which uses the pound sponge and dough method (PSD) as the bread baking method of choice. This study is to compare the baking results among PSTD, PSD, and pup sponge and dough method, and to find out if baking results from PSTD could be used for predicting baking results from other two methods. We used 47 flours (26 HRRW and 21 HRSW) from Wheat Quality Council grown in 2002. Significant correlations were observed in crumb grain score ($r = 0.58$, $P < 0.0001$) and loaf volume ($r = 0.85$) between PSTD and PSD. Predicting equation for loaf volume of PSD was obtained ($R^2 = 0.92$) by stepwise multiple regression analysis using baking parameters of PSTD. Considering longer process and larger amount of flour required for PSD, PSTD is fast, simple, yet potent method. Pup sponge and dough method is under investigation.

Physical and chemical characterization of wheat flour milling coproducts.

Y.S. Kim, R.A. Flores, O.K. Chung, and D.B. Bechtel.

The first step in food product formulation and development is the characterization of the raw materials. This basic understanding of the properties of the raw materials permits improvement of the products and the development of new products. This study compared the properties of HRWW and HRSW milling coproducts such as bran, germ, shorts, and

red dog. The properties studied included true and bulk density size, proximate analysis (protein, ash, lipid and fiber), and thermal properties (thermal conductivity and specific heat). All properties were determined for samples originating in different commercial and pilot plant mills. The results of this study update previous characterization studies and fill in the information gaps for wheat milling coproducts not previously available. Hard red winter and HRSW milling coproducts (bran, germ, shorts, and red dog) from three commercial flour mills and the Kansas State University pilot mill were evaluated for differences in physical, chemical, and thermal properties. The true and bulk densities of coproducts were significantly ($p < 0.05$) related to the moisture content (R^2 of 0.913–0.999 and 0.817–0.999 for true and bulk densities, respectively). The red dog had the smallest geometrical mean diameter with the highest variation (coefficient of variation of 23.8 %). The average thickness of bran and germ particles measured with image analysis was significantly different ($p < 0.05$) among separation sizes, different wheats, and milling flows. Chemical compositions (protein, ash, fiber, and lipid) of coproducts in this study were within the range of published data. Thermal conductivity measured with the line source technique was significantly related to moisture content of the sample, with R^2 ranging from 0.740 to 0.998. Specific heat of coproducts, measured with a differential scanning calorimeter exhibited a wider range (1.08 - 1.94 kJ/kgK) than that observed in whole wheat kernels and wheat flour. The variability observed among the samples was due to different sources of wheat and characteristic milling flows for the flour mills.

Application of NIR for rapid wheat quality analysis.

B.W. Seabourn and O.K. Chung.

Since the development of the first computerized NIR spectrometer by Ben-Gera and Norris (USDA) in 1968 for the measurement of moisture in meat products, NIR spectroscopy has seen unprecedented growth in its use, not only in agricultural products, but also in many different and widely varying scientific disciplines and commercial applications, due in large part to its unrivaled combination of simplicity, accuracy, and speed of analysis. Today, there are literally thousands of NIR spectrometers in use worldwide. NIR spectroscopy has become a widely used method in food analysis and the quality evaluation of agricultural products because it is a highly flexible, low-cost, intrinsically safe, rapid, and, in most cases, nondestructive technique in which very little, if any, sample preparation is required. NIR has the added advantages of multiconstituent analysis in which no by-products or hazardous materials are generated. Increased competition, expanding markets, development of new products, and issues of quality control, segregation, and safety are just a few of the demands facing the wheat industry around the world. The application of NIR spectroscopy to these issues and the evaluation of wheat quality are reviewed.

A method for monitoring the rheology and protein secondary structure of dough during mixing using FT-HATR spectroscopy.

B.W. Seabourn, O.K. Chung, P.A. Seib, and P.R. Mathewson.

An infrared spectroscopic method was developed to determine changes in the secondary structure of gluten proteins in a flour-water dough system as it was mixed. FT-HATR mid-infrared spectra of mixed doughs revealed changes in four bands in the amide III region typically associated with secondary structure of proteins: 1,317 (a-helix), 1,285 (b-turn), 1,265 (random coil), and 1,242 cm^{-1} (b-sheet). The largest band, which also showed the greatest change in second derivative band area (SDBA) during mixing (increasing over time), was the band at 1,242/ cm . The bands at 1,317, 1,285, and 1,242/ cm also showed an increase in SDBA over time. Alternatively, the band at 1265/ cm showed a corresponding decrease during mixing. All bands reached an optimal (or minimal) corresponding to the optimum development of the dough. Increases in a-helical, b-turn, and b-sheet structures during mixing suggest that the secondary structure of gluten protein assumes a more ordered conformation, apparently at the expense of random coil structure in the macromolecule. These results demonstrate that it is possible to follow the rheological behavior of dough based on changes in the protein structure of the system.

Spelt quality and starch chemistry.

J.D. Wilson, D.B. Bechtel, and P.A. Seib.

Spelt is an old-world hexaploid, hulled wheat that has recently received renewed interest in the USA. There have been few reports on test baking of spelt wheat flour into bread nor of its starch properties. Five spelt wheats were micro-milled into flour (~70 % extraction) and test baked. Quality factors such as; proteins (8.7–12.7 %), bake mix time (2.25–11 min), crumb score (0.5–4.75) and loaf volume of 10-g bakes (42–77°C) were measured. Starch was isolated by protease digestion from flour and evaluated for total starch (75–82 %), starch damage (2.3–3.2 %), and amylase content (30–33 %). Thermal properties of isolated starch were conducted by differential scanning calorimetry to obtain gelatinization profiles ($T_o = 53\text{--}58^\circ\text{C}$; $TP = 63\text{--}66^\circ\text{C}$; $TC = 70\text{--}73^\circ\text{C}$; $\Delta H = 8\text{--}13\text{ J/g}$) as well as disassociation of amylase/lipid complexes ($T_o = 85\text{--}89^\circ\text{C}$; $TP = 97\text{--}100^\circ\text{C}$; $TC = 102\text{--}106^\circ\text{C}$; $\Delta H = 1.3\text{--}1.7\text{ J/g}$). Isolated starch showed unique differences compared to HRWW with respect to the initial peak (192–229 RVA) and final viscosity (161–297 RVA) using the Rapid Visco Analyzer. This study revealed spelt starch to have lower starch damage and higher amylase content than the hard red winter wheat control.

Effect of temperature on expression of genes encoding enzymes for starch biosynthesis in developing wheat endosperm.

W.J. Hurkman, K.F. McCue, S.B. Altenbach, A.M. Korn, C.K. Tanaka, K.M. Kothari, D.B. Bechtel, J.D. Wilson, O.D. Anderson, and F.M. Dupont.

High temperature during grain-fill reduces yield in wheat. The reduction in yield is caused by a decrease in total starch content of the grain. We studied the effect of high temperature on starch accumulation, the relative number and volume of starch grains, and the expression of key genes for the starch biosynthetic pathway were examined during grain development. Maximum starch weight was attained earlier in grain of plants grown under high temperatures and total starch weight was much less in the mature grain. High temperatures also changed the relative number and volume of the three different starch granule size classes found in the grain. Messenger RNA levels for starch biosynthetic enzymes peaked early in development and decreased substantially, especially the messenger RNA for soluble starch synthase. These findings demonstrate that high temperatures influence not only starch synthesis, but also the overall developmental program for grain development. The effect of high temperature on starch accumulation, starch granule populations, and expression of genes encoding key enzymes for starch biosynthesis was examined during grain development in wheat cultivar Butte 86. High temperature applied from anthesis to maturity reduced the duration of starch accumulation. Starch accumulation ceased ~ 6 days earlier for grain produced under a 37/17°C (day/night) regimen and 21 days earlier under a 37/28°C (day/night) regimen than for grain produced under a 24/17°C (day/night) regimen. Compared to the 24/17°C regimen, starch content was ~ 19 % less for mature grain produced under the 37/17°C regimen and 58 % less under the 37/28°C regimen. The smaller type-B starch granules were the predominant class in mature grain produced under the 24/17°C and 37/17°C regimens, based on relative volume, whereas the larger type-A granules were predominant in grain produced under the 37/28°C regimen. Under the 24/17°C regimen, steady state transcript levels for ADP-glucose pyrophosphorylase, starch synthases I, II, and III, granule-bound starch synthase, and starch branching enzymes I and II were highest from 12–16 days post-anthesis. Under the 37/17°C regimen, steady state levels of these transcripts followed the same temporal pattern, but were substantially lower. Under the 37/28°C regimen, transcript levels peaked earlier, at 7 days post-anthesis. The high temperature regimens reduced the relative levels of transcripts for starch synthase more than the other starch biosynthetic enzymes.

HPLC of gluten monomeric proteins.

G.L. Lookhart, S.R. Bean, and J.A. Bietz.

High performance liquid chromatography is an analytical method that uses a liquid pumping system to accurately deliver solvents through a column or columns each packed with particles of a specific size (1.5–10 μm) and with specific bonded phases. The end result is the ability to separate complex mixtures in minutes. HPLC is a superb tool as it is complementary and often superior to previous methods for characterization of complex cereal proteins. Reversed-phase and ion-

exchange HPLC separations of gluten monomers and the hundreds of reports that describe such studies were summarized with references to more comprehensive reviews and provides protocols for these separations.

Reversed-phase high performance liquid chromatography in grain applications.

G.L. Lookhart, S.R. Bean, and J.A. Bietz.

High-performance liquid chromatography uses a liquid pumping system to accurately deliver solvents through a column packed with 1.5–10- μ m particles with specific bonded phases. The end result is the ability to separate complex mixtures in minutes. We have focused on the separation of gluten monomers using reversed-phase HPLC (RP-HPLC). RP-HPLC is a method often used for gluten protein analysis, its resolution equals or exceeds that of most other methods, and it is fast, reproducible, sensitive, quantifiable, and gives good recovery. Most importantly, however, it complements other methods, since it fractionates proteins on the basis of different surface hydrophobicities.

Wheat varietal identification and wheat quality.

G.L. Lookhart and S.R. Bean.

The ability to identify wheat at all stages of its growth and use is very important. Quality is in the eye of the beholder! A farmer might define quality as the amount of grain produced in the field, a miller might define it as the amount of flour that can be produced from a bushel of wheat on a given mill, a baker might define it as the type of consistent product that can be made from a given flour, and a breeder might define it as the overall resistance to disease, the grain yield, and the utilization of the grain by various end users. In each of these definitions, genetic, environmental, and 'genetic x environmental' components are present. Because we cannot control the environment, controlling or identifying the genetics is important. Wheat gliadins are a genotypic expression of the plant and, therefore, characterization of the gliadins can be used to fingerprint wheat genotypes. Cultivar identification can be accomplished in any of three broad ways: agronomic, physical, or biochemical. We have described and compared each of these areas and focused on the biochemical methods of electrophoresis and chromatography to characterize or fingerprint wheat proteins for varietal identification.

Wheat flour proteins as affected by transglutaminase and glucose oxidase.

C.M. Rosell, J. Wang, S. Aja, S.R. Bean, and G.L. Lookhart.

Enzymes are good tools to modify wheat proteins by creating new bonds between the protein chains. We studied the effect of the addition of glucose oxidase and transglutaminase on the wheat flour proteins. The modification of wheat proteins was determined by analyzing the changes in gluten quality, alveograph parameters, and protein modifications. The amount of wet gluten increased with the addition of glucose oxidase and transglutaminase, but the gluten quality was not improved in any case. Regarding the alveograph parameters, the effect of glucose oxidase was readily evident obtaining wheat dough with higher tenacity and lower extensibility than the control, whereas transglutaminase led to doughs with lower tenacity and that were also less extensible. The protein modifications were characterized by free-zone capillary electrophoresis (FZCE). FZCE data indicated that transglutaminase polymerizes mainly glutenins and, of those, the high molecular weight glutenin subunits were the most affected.

Methods for analyzing polymeric proteins of wheat their impact on wheat quality.

S.R. Bean and G.L. Lookhart.

The polymeric proteins of wheat have been found correlated to wheat quality attributes such as mixing strength. Improved methods for characterizing these proteins were developed and applied to the study of wheat quality. A rapid method for measuring the amount of insoluble polymeric protein was developed based on short, multiple extractions with 50 % 1-propanol followed by nitrogen combustion analysis. Good correlations between dough strength parameters and amounts of pellet protein and percent pellet protein (pellet protein/flour protein) were found for all samples. This

procedure was found to be simple and rapid, with the potential of analyzing over 100 samples/day with good reproducibility. In addition, a method was developed to measure the actual size distribution of the polymeric proteins. This method used multi-angle laser light scattering (MALLS) in conjunction with size exclusion chromatography (SEC). Four solvent systems for analyzing wheat gluten proteins by MALLS were evaluated for use in extraction and as SEC mobile phases. The dn/dc values for wheat proteins were measured in each solvent. Although all solvents showed similar resolution when used as mobile phases in SEC analysis, the SDS solvent extracted the most protein (~82 %) in the unreduced form. This solvent system also displayed no concentration dependent or electrostatic effects during MALLS analysis. The SDS-soluble and -insoluble protein complexes were characterized by MALLS and Mw distributions ranging up to 8.1×10^6 Da were found for the insoluble SDS-protein complexes. The effect of the column void volume was also examined as was data analysis parameters such as fitting method and peak placement. This method could be used to measure the size distribution of polymeric proteins in wheats differing in quality.

Glutenin particles are affected by growing conditions.

C. Don, G.L. Lookhart, H.A. Naeem, F. MacRitchie, and R.J. Hamer.

Wheat quality is governed by both genetic and environmental factors. The glutenin macro-polymer particle gel (GMP), is recognized as a key to better understand flour quality. The formation of glutenin particles and how they are affected by growing conditions was studied. The NILs Lance C (5+10) + Lance A (2+12) and Warigal A (5+10) + Warigal B (2+12) were used. The wheat lines were grown under controlled conditions, using various temperature regimes to simulate stress effects. GMP quantity in the flours varied with heat treatments, suggesting a link between total GMP quantity and stress. Typical GMP particle size distributions (PSD) for the flours in ~10–200 μm range could be observed with Coulter Laser. Wheat stressed 40°C day/25°C night for 16 days after anthesis had a much lower quantity of GMP. However, we still observed a narrow PSD-peak indicating that large size GMP particles are still present in heat stressed samples. When wheat was heat-stressed at a later stage, 40/25°C - 25 days after anthesis, more GMP was recoverable and glutenin PSD was broader. Lines with 5+10 contained larger particles than those with 2+12. More interesting findings on GMP and PSD are GMP, genetics, heat-stress, protein composition, and flour quality.

Separation of water soluble proteins from cereals by high performance capillary electrophoresis.

M. Tilley and S.R. Bean.

Most research concerning grain proteins has concentrated upon the gluten storage proteins. The albumins and globulins are the water- and salt-soluble proteins that contain biologically active enzymes and enzyme inhibitors. A free zone capillary electrophoresis method was developed to separate these proteins. Optimization included sample extraction method, capillary temperature, buffer composition, and additives. The optimal conditions for separation of these proteins was found to be 50 μm i.d. x 27 cm (20 cm to detector) capillary at 10 kV (with a 0.17 min ramp up time) and 25°C. The optimum buffer was 50 mM sodium phosphate, pH 2.5 + 20 % acetonitrile (v/v) (ACN) + 0.05 % (w/v) hydroxypropylmethyl-cellulose (HPMC) + 50 mM hexane sulfonic acid (HSA). Sample stability was an issue that was addressed by lyophilizing fresh extracts and redissolving in aqueous 50 % ethylene glycol and 10 % separation buffer. This method was successfully used in both wheat flour and whole meal samples. Comparisons were made of several wheats of different classes as well as several cereal grains. This methodology could be useful in screening cereal grains for important enzymes and their impact on end-use quality such as food functionality, food coloration, and malting quality.

Tyrosine crosslink formation in wheat dough: innate enzymatic activity.

M. Tilley and K.A. Tilley.

Formation of the 3-dimensional protein network known as gluten during dough mixing and bread making processes is extremely complex. Evidence presented here indicates that tyrosine bonded species form in wheat doughs during the processes of mixing and baking and are major contributors to the structure of the gluten network. Various oxidizing and reducing agents that have been used in the baking industry directly affect tyrosine bonds. Tyrosine bonds between

synthetic glutenin peptides form in vitro under baking conditions in the presence of potassium bromate and in the presence of water-soluble extract of flour. Bond structures and formation during bread-making processes have been documented by HPLC, NMR, and mass spectroscopic analyses. The formation of tyrosine crosslinks in developing wheat kernels also has been documented, shedding light on the biological mechanisms for tyrosine crosslink formation. Innate enzymes in the endosperm (flour) of wheat kernels have been isolated and characterized. Information regarding these enzymes and their ability to form dityrosine during bread-making processes will be described. These enzymes and their functions provide necessary points of control during bread-making processes.

Wheat protein subclasses in relation to characteristics of experimental pup-loaf breads.

S.H. Park, O.K. Chung, P.A. Seib, and S.R. Bean.

Flour proteins were extracted from 49 hard winter wheat flours with 50 % 1-propanol. The soluble proteins (SP) were separated into albumin/globulin (AG), gliadins, and soluble polymeric protein (SPP) fractions using SEC-HPLC. Insoluble polymeric proteins (IPP) were determined by nitrogen combustion using a LECO FP-428 nitrogen determinator. Flour protein content (FPC) was highly correlated to loaf volume (LV, $r = 0.82$, $p < 0.0001$) and dough proof height (DPH, $r = 0.74$, $p < 0.0001$); SP amount was highly correlated to FPC and LV as well ($r = 0.85$ and $r = 0.74$, respectively) as was gliadin ($r = 0.73$ and $r = 0.71$, respectively). IPP amount was correlated to bake water absorption (BWA, $r = 0.62$, $p < 0.0001$) as well as FPC ($r = 0.45$, $p < 0.005$). Bake mix time (BMT) was not correlated to FPC, due to the opposite effects shown by IPP and SP, i.e., BMT was positively correlated with IPP ($r = 0.86$) but negatively correlated with SP ($r = -0.75$) and gliadins ($r = -0.43$). Bread crumb grain scores (CGS) were correlated positively with SP and gliadin amounts ($r = 0.35$ and 0.30 , respectively, $p < 0.05$) but negatively with AG % protein ($r = -0.40$) and AG/SP ratio ($r = -0.41$). Thus, SP amount and gliadins affected LV, DPH, and CGS positively but BMT negatively, whereas IPP affected BWA and BMT positively. The percent protein of AG and IPP had negative correlations with LV and DPH.

Free tryptophan in wheat grain and milling fractions.

L.M. Seitz, and M.S. Ram.

Relatively little information is available on free amino acids in whole wheat or milling fractions. In this research, we focused on the essential amino acid tryptophan, which we found could be readily extracted with methanol from ground whole wheat and wheat milling fractions. Extracts were analyzed by HPLC using UV-Vis and fluorescence detectors. Retention time and spectra (UV-Vis and fluorescence) of the component from samples were equivalent to those from a tryptophan standard. Derivatization with dansyl chloride and ninhydrin also aided identification. From analysis of methanol extracts of ground wheat, tryptophan concentrations were about 12 and 35 $\mu\text{g}/\text{gram}$ for cultivars Scout 66 and Trego, respectively, grown near Bushland, TX, in 2002. Germination of these cultivars for about 3 days increased the tryptophan concentration slightly. With milling fractions, free tryptophan was present in bran and shorts at levels about 10 times higher than in flour. Analyses for free tryptophan in selected cultivars from known locations could provide information on factors such as type of wheat and environment during grain maturation that may influence the level of this important amino acid in wheat grain.

Natural fluorescence of red and white wheat kernels.

M.S. Ram, L. Seitz, and F.E. Dowell.

For marketing purposes, red and white wheat need to be kept segregated because mixtures of these wheats are discounted, and some have different end uses. Identification of wheat color class is not straightforward, and currently, characterizing red and white wheat using spectroscopy and chemical tests is of great interest. During preliminary observations, we noticed that all varieties of red and white wheat exhibited natural fluorescence under UV light in a viewing cabinet, and there appeared to be some differences between red and white wheats. From a study of 90 cultivars (41 red and 49 white), we found that fluorescence emission spectra of red wheat kernels are different from those of white wheats, as indicated by partial least-squares and neural networks analysis. This information may aid development of a

simple, rapid wheat color class identification process easily without the use of chemicals. Only a relatively inexpensive spectrofluorometer would be required, and the test may be extendable to single kernels.

Improving wheat quality.

O.K. Chung, S.H. Park, M. Tilley, and G.L. Lookhart.

This is a chapter of a book “Breadmaking: Improving Quality” edited by S.P. Cauvaine, published by the Woodhead Publishing Company.

On average, for three recent years (1998–99 through 2000–01), the U.S. produced 64.2×10^6 metric tons (mmt) of wheat representing about 11 % of the world production. Wheat is the most valuable food crop and the major export crop of the U.S., as 43 % (28.8 mmt) enters the export market. The U.S. produces several classes of wheat which have different functional properties and end-uses. The major bread wheat classes, HRWW and HRSW, comprise 63–65 % of total U.S. wheat production and 62–63 % of U.S. wheat exports. Official U.S. Standards for Wheat and established and maintained by the U.S. Department of Agriculture.

Wheat quality improvement begins with breeding. Important traits targeted in wheat breeding include both agronomic and end-use qualities. The USDA, Agricultural Research Service maintains four Regional Wheat Quality Laboratories that have made paramount contributions to U.S. wheat improvement for all wheat classes. Quality evaluation in the U.S. bread wheat-breeding program was once limited to traditional milling and bread-baking tests and is now rapidly expanding to include a wider range of tests for multiple end-use products. Tremendous growth exists in nontraditional uses, such as Asian products, noodles, frozen dough, par-bake products, tortillas, and pizza crust. To take full advantage of these expanding markets, new quality parameters and quality prediction tests are being developed for breeding programs and commercial wheat cultivars. Quality evaluation is a valuable approach in retaining a competitive edge in world markets while addressing new demands of domestic customers.

Functional properties of waxy wheat flours: Genotypic and environmental effects.

R.A. Graybosch, E. Souza, W. Berzonsky, P.S. Baenziger, and O.K. Chung.

Alternative uses of our most common grain crops often is cited as a necessity for the development of a more sustainable agricultural system, and a means of salvation for rural economies. After many years of discussion, a well-defined alternative use of common wheat now is in sight. Waxy (amylose-free) wheats have a modified starch structure that will allow wheat starch to be used in a number of novel food and industrial applications. Waxy spring wheats were developed via traditional crossbreeding of lines carrying natural mutations that interrupt the synthesis of amylose, a natural component of wheat starch. The resultant starch consists only of amylopectin, another natural component. Waxy wheats, then, are 100 % natural and nonGMO. The change in starch structure conferred different cooking properties to the waxy wheats. The cooking properties were remarkably stable over diverse cultural environments. Grain yield of the highest yielding spring waxy wheats was not significantly different from that of normal spring wheat cultivars included as controls. The study demonstrates that waxy wheats can be developed that will not carry a penalty in grain yield, that waxy wheats have unique functional properties, and that these functional properties are extremely resistant to modification by environmental factors. Commercial firms interested in using waxy wheats will be able to obtain consistent raw materials from diverse environments. A set of waxy (amylose-free) experimental spring wheats of diverse parentage were grown, along with two nonwaxy and two partial waxy check cultivars, at diverse North American cultural environments. Grain yield and functional attributes of derived flours were determined. Average grain yield of the waxy lines did not differ significantly from the average yield of the check cultivars, but significant differences were observed amongst the waxy lines. Grain hardness varied significantly among the waxy lines, and both hard and soft textured waxy lines were identified. Analysis of flour quality traits showed few differences between waxy lines and check cultivars for traits primarily related to protein concentration or protein quality, but many significant differences between properties primarily dependent upon starch structure, or related to milling behavior. Protein-related quality attributes of waxy wheats demonstrated environmental and genotypic variances similar to those typical of nonwaxy wheats. Starch-related quality attributes of waxy wheats showed remarkable stability across environments, but some significant genetic variation was

observed. End-users interested in employing waxy wheats should be able to select desired waxy lines, and feel confident that the starch-related functional properties will be environmentally stable.

Genetic, agronomic, and quality comparisons of two T1AL·1RS wheat–rye translocations.

R.A. Graybosch, J.H. Lee, C.J. Peterson, D.R. Porter, and O.K. Chung.

The T1AL·1RS wheat–rye translocation originally found in Amigo wheat possesses resistance genes for stem rust, powdery mildew, and greenbug biotypes B and C, also has a negative effect on wheat processing quality. Recently, a second T1AL·1RS translocation with *Gb6*, a gene conferring resistance to greenbug biotypes B, C, E, G, and I, was identified in the wheat germ plasm line GRS1201. Protein analytical methods and PCR were used to identify markers capable of differentiating the 1RS chromosome arms derived from Amigo and GRS1201. The secalin proteins encoded by genes on 1RS chromosome arms differed in Amigo and GRS1201. A secalin of Mr 70 kD was found in the Amigo T1AL·1RS but did not occur in the GRS1201 T1AL·1RS. Polymorphisms detected by PCR primers derived from a family of moderately repetitive rye DNA sequences also differentiated the two translocations. When GRS1201 was mated with a non-1RS wheat, no recombinants between 1RS markers were observed. Recombination between 1RS markers did occur when 1RS from Amigo and 1RS from GRS1201 were combined, but in such intermatings, the molecular markers described herein could still be used to develop a population enriched in lines carrying *Gb6*. No differences in grain yield or grain and flour quality characteristics were observed when lines carrying 1RS from Amigo were compared to lines with 1RS from GRS1201. Hence, differences in secalin composition did not result in differential quality effects. When compared to sister lines with T1AL·1AS derived from the wheat cultivar Redland, lines with GRS1201 had equal grain yield but produced flours with significantly shorter mix times, weaker doughs, and lower SDS sedimentation volumes.

Release of N95L11881 and 95L9521 strong gluten T1BL·1RS wheats.

R.A. Graybosch, C.J. Peterson, and O.K. Chung.

N95L11881 (PI 617064) and **95L9521** (PI 617066) HRWW were released by the Agricultural Research Service, United States Department of Agriculture, and the Nebraska Agricultural Experiment Station, in June, 2002. These lines carry the T1BL·1RS wheat–rye chromosomal translocation inherited from the HRWW Siouxland, but they possess improved gluten strength relative to this parent. The T1BL·1RS translocation in Siouxland originally was derived from the Russian wheat Kavkaz. Although this translocation confers a number of advantageous traits, including resistance to several fungal diseases and improved grain yield and grain yield stability, it has a detrimental effect on the processing quality of hard winter wheats. The most noticeable effect, a lack of dough strength, is overcome in these two germ plasm lines.

Registration of N96L9970 Greenbug resistant wheat.

R.A. Graybosch, C.J. Peterson, D.R. Porter, and O.K. Chung.

N96L9970 is a HRWW germ plasm line developed coöperatively by the United States Department of Agriculture, Agricultural Research Service, and the Nebraska Agricultural Experiment Station, and was released in June, 2002. N96L9970 carries resistance to multiple biotypes of greenbug. N96L9970 (PI 619231, GRS1201/TAM-202) is resistant to greenbug biotypes B, C, E, G, I, and K. GRS1201 carries a T1AL·1RS wheat–rye chromosomal translocation originally produced from an irradiated alien chromosome substitution plant derived from a wheat/rye hybrid (short wheat selection/Scout (TX69A345-2)/Insave rye/3/TAM101). TAM-202 (described as an outcross between an unknown parent and Siouxland) has a different T1AL·1RS translocation. The greenbug resistance of N96L9970 is located on the T1AL·1RS translocation inherited from GRS1201. N96L9970 primarily was released due to significant agronomic performance relative to GRS1201, the only previously released source of resistance to greenbug biotypes B, C, E, G, I, and K.

Release of nineteen waxy spring wheats.

R.A. Graybosch, E. Souza, W. Berzonsky, P.S. Baenziger, D.V. McVey, and O.K. Chung.

Nineteen spring waxy (amylose-free) wheat germ plasm lines were developed and released by the Agricultural Research Service, United States Department of Agriculture, and the Nebraska Agricultural Experiment Station in cooperation with the Agricultural Experiment Stations of North Dakota and Idaho. Waxy wheats carry three nonfunctional (null) alleles (*Wx-A1b*, *Wx-B1b*, and *Wx-D1b*) at the genetic loci encoding the enzyme granule-bound starch synthase (GBSS, EC 2.4.1.21). GBSS also is known as the waxy protein. Waxy wheats produce endosperm starch that is nearly devoid of amylose. Such starch confers unique functional properties to derived wheat flour. Suggested uses for waxy wheats include the production of modified food starches, a blending agent to create flours with optimal amylose concentration for the production of a variety of sheeted and baked food products, and as an animal feed. Waxy wheats also are useful as donors of the *Wx* null alleles, which may be used to develop partial waxy or reduced-amylose wheats. The presence of one or two such alleles can result in wheat flours with superior performance in certain food applications.

Registration of Ankor wheat.

S.D. Haley, J.S. Quick, J.J. Johnson, F.B. Peairs, J.A. Stromberger, S.R. Clayshulte, B.L. Clifford, J.B. Rudolph, O.K. Chung, and B.W. Seabourn.

Ankor HRWW was developed by the Colorado Agricultural Experiment Station and released to seed producers in August 2002. Ankor was released because of its resistance to the RWA and adaptation for dryland production in eastern Colorado and the west central Great Plains. Ankor was selected from the crosses and backcrosses 'Akron/Halt//4*Akron' made between 1994 and 1998. Halt (PI 584505) and Akron (PI 584504) are cultivars released by Colorado State University in 1994. Ankor is resistant to stem rust, susceptible to leaf rust, and susceptible to both WSMV and BYDV and Hessian fly and greenbug, and resistant to RWA. Ankor was tested in 11 trial locations of the dryland Colorado during from 2001 to 2002 (2,647 kg/ha) and had a similar yield as Prairie Red (2,620 kg/ha; $P > 0.05$) and less than Akron (2,714 kg/ha; $P > 0.05$). Relative to its recurrent parent Akron, Ankor had higher grain volume weight (727 versus 721 kg/m³), kernel weight (24.8 versus 23.6 mg/kernel), and percent large kernels (36.3 versus 27.5 % kernels that do not pass a Tyler #7 sieve, 2.92 mm openings). Flour protein and ash contents, dough mixing properties, flour, and bread-making properties were similar to those for Ankor and Akron. The Colorado Agricultural Experiment Station will maintain breeder seed of Ankor. Ankor has been submitted for U.S. Plant Variety Protection under P.L. 91-577 with the certification option. Ankor was developed with financial support from Colorado Agricultural Experiment Station Projects 795 and 646, the Colorado Wheat Administrative Committee, and the Colorado Wheat Research Foundation.

Using visible and near-infrared reflectance spectroscopy and differential scanning calorimetry to study starch, protein, and temperature effects on bread staling.

F. Xie, F.E. Dowell, and X.S. Sun.

Bread staling is a complex process that occurs during bread storage and is a progressive deterioration of quality such as taste, and firmness. The mechanism of bread staling is still not clear yet, even though it has been studied for 150 years. Starch, protein, and temperature effects on bread staling were investigated using visible and NIR spectroscopy and differential scanning calorimetry. The potential of NIR spectroscopy in studying bread staling was investigated. The results show that starch, protein, and moisture all contributed to the bread staling process. Bread staling mainly was due to amylopectin retrogradation; amylopectin reformed into double helical structure and recrystallized. The amylose-lipid complex changed little one day after baking. Low temperature dramatically accelerated the amylopectin retrogradation process. Protein retarded bread staling but not as much as temperature. The starch and protein interaction was less important than the starch retrogradation. Protein hindered the bread staling process mainly by diluting starch and retarding starch retrogradation. NIR spectroscopy measured amylopectin retrogradation accurately in different batches. NIRS followed moisture and starch structure changes when measuring retrograded amylopectin. Five important wavelengths, 550, 970, 1,155, 1,395, and 1,465 nm, indicates that NIR spectroscopy could provides information on starch, protein, moisture, and color. The results of this study could lead to solutions of reducing bread staling that will bring

great economic benefit to both of bakers and consumers in the future. In addition, the results will be helpful in developing NIR spectroscopy applications further as a means for studying bread staling or other similar phenomenon.

Comparison of near-infrared reflectance spectroscopy and a texture analyzer for predicting wheat bread staling.

F. Xie, F.E. Dowell, and X. Sun.

Bread staling affects bread texture properties and is one of the most common problems in bread storage. Bread firmness, as measured in compression mode by a texture analyzer (TA), has been commonly used to measure bread staling. This study investigated the potential of visible and NIR spectroscopy to detect bread changes during storage by comparing NIR spectroscopy results with those obtained by the TA. Twenty-five loaves of commercial wheat white pan bread from one batch were studied over 5 days. NIR spectroscopy and TA measurements were made on the same slice at approximately the same time. The experiment was repeated five times using the same kind of commercial samples from five different batches. NIR spectroscopy measurements of slices, loaf averages, and daily averages were compared with TA measurements. NIR spectroscopy spectra had high correlation with TA firmness. NIR spectroscopy measurements correlated better with the actual storage time and had smaller standard deviations than the TA measurements. The batch differences had less effect on NIR spectroscopy measurements than on the TA measurements. The results indicate that NIR spectroscopy could follow bread changes during storage more accurately than TA. NIR spectroscopy is probably based on both physical and chemical changes during bread staling, unlike the TA method that only measures bread firmness, which is only one aspect of the staling phenomenon.

Measuring wheat hardness by single-kernel visible and near-infrared reflectance spectroscopy.

E.B. Maghirang and F.E. Dowell.

Wheat hardness is a primary quality trait that relates wheat to its milling properties and end-use quality. The current standard measurement techniques for wheat hardness are destructive, i.e., they require grinding or crushing of wheat samples. A measurement technique, such as in breeding programs, that is nondestructive, rapid, accurate, and that requires small sample sizes is needed. A commercially available single-kernel, visible and NIR reflectance (VisNIR) spectrometer (Single Kernel Characterization System 4170) was used to develop a bulk-hardness measurement and wheat-classification technique. This technique requires only 30 whole single kernels, which can be automatically and nondestructively processed using VisNIR, for a total run time of only 30 seconds. This technique predicted hardness values with 83 % accuracy and correctly classified wheat as soft, hard, or mixed wheat with 100 % accuracy. The potential of using VisNIR may be attributed to the apparent capability of this technique to distinguish between the strength of adhesion between starch and protein, which varies across hard and soft wheats and also may be possibly related to the extent of the level of relationship between hardness and vitreousness. VisNIR using whole kernels has already proven effective for measuring numerous grain attributes such as protein, moisture content, vitreousness, color class, internal insects, and bunt. VisNIR instruments being used to measure these attributes can be used for grain hardness measurement and hardness classification. As such, this may reduce the number of instruments and/or steps required for evaluating grain attributes. The demand for instruments that can measure multiple attributes that are essential for determining end-use quality will increase, especially true with the shift in the wheat industry to being an end-use oriented market. Likewise, wheat breeding programs are expected to benefit from this technique considering its nondestructive feature, small sample size requirement, accuracy, and rapidity.

Granulation sensing of first-break ground wheat using a near-infrared reflectance spectrometer.

M.C. Pasikatan, E. Haque, C.K. Spillman, J.L. Steele, and G.A. Milliken.

Currently, we have very little automation in wheat mills. If the roll gap setting was automated, then the efficiency of the mills can possibly be improved. A NIR reflectance spectrometer was evaluated as a potential granulation sensor because of the known relationship of NIR reflectance to the particle size of ground products. Six wheat classes were ground

using five roll gaps of a first-break roller mill. Good correlations were achieved between the larger granulation sizes and NIR reflectance. The granulation sensing technique based on NIR reflectance is ready for online evaluation.

Granulation sensing of first-break ground wheat using a near-infrared reflectance spectrometer: studies with soft red winter wheats.

M.C. Pasikatan, E. Haque, C.K. Spillman, J.L. Steele, and G.A. Milliken.

A sensor for granulation could change roll gap settings automatically to follow changes in granulation of ground wheat, unlike the operator-fixed setting of present roller mills. A fully automated roller mill could help optimize flour extraction in flour-milling systems. Previously, we studied the feasibility of developing a granulation sensor out of a NIR reflectance spectrometer, using ground wheat from six wheat classes and HRWWs. This time, we studied ground wheat from SRWW. Two sets of 35 wheat samples, representing seven SRWW cultivars, were ground independently using five roller mill gaps (0.38, 0.51, 0.63, 0.75, and 0.88 mm). NIR reflectance of one set was used to develop calibration to estimate granulation from spectral data of the other set. Granulation models based on partial least squares regression were developed with cumulative mass of size fractions as reference value. Different ways of treating the spectral data (log (1/R), baseline correction, unit area normalization, and derivatives) and subregions of the 400–1,700 nm wavelength range were evaluated. Models that corrected for path length effects (those that used unit area normalization) predicted the bigger size fractions well. The model based on unit area normalization-first derivative predicted 34 out of 35 validation spectra with square root of the sum of squared differences between reference and predicted data of 3.53, 1.83, 1.43, and 1.30 for the >1,041, >375, >240, and >136 μ m size fractions, respectively. The SRWW granulation models performed better than the previously reported models for six wheat classes owing to less variation in mass of each size fraction. However, SRWW flour has tendency to stick to the underside of sieves that affected the reference values. Thus the finest size fraction of these models did not perform as well as the HRWW models.

High-speed segregation of high- and low-protein single wheat seeds.

M.C. Pasikatan and F.E. Dowell.

High protein content is preferred in wheat products such as pasta while low protein content is desirable for cakes and cookies. Wheat with higher protein commands higher price (about 5 cents more per bushel) in export markets. A specific protein content range is one of the goals of wheat breeding programs but breeders, currently, do not have a nondestructive method to rapidly screen single wheat kernels for protein content. We evaluated the potential of a commercial high-volume color sorter for this purpose. The sorter was equipped with NIR optical filters and sensors for this application. Wheat blends that approximated the low- and high-protein range of early generation wheat populations were obtained by mixing high protein (protein content > 12.5 % at 12 % moisture basis) and low-protein (protein content <11.5 %) wheat from hard red winter and hard white wheat varieties in proportions of 50:50 and 95:5 % mass. The sorter was set to either reject high- or low-protein wheat kernels. Wheat blends were then passed through the sorter five times where each pass removed 10% of the wheat mass. The bulk protein content of accepted kernels (accepts) and rejected kernels (rejects) were measured for each pass. For 50:50 blends, higher changes in protein content (about 1 %) relative to the original sample could be obtained from the first-pass rejects instead of the fifth-pass accepts (about 0.5 %). Two resorts of accepts would be needed to move 95:5 blends toward the direction of the dominant protein content. The sorter has potential to help breeders in shifting early generation wheat populations toward the target protein level. At this level of technology, sorting was partly driven by color and vitreousness differences between high- and low-protein wheat.

Detection of insect fragments in wheat flour by near-infrared spectroscopy.

J. Perez-Mendoza, J.E. Throne, F.E. Dowell, and J.E. Baker.

Primary pests of stored cereals that develop and feed inside grain kernels are the main source of insect fragments in wheat flour. The Food and Drug Administration (FDA) has set a defect action level of 75 or more insect fragments/50

gram of flour. The current standard flotation method for detecting insect fragments in flour is very labor intensive and expensive. We investigated the potential of near-NIR spectroscopy to detect insect fragments in wheat flour at the FDA defect action level. Fragments counts with both the NIR spectroscopy and the standard flotation methods correlated well with the actual number of fragments present in flour samples. However, the flotation method was more sensitive below the FDA defect action level than the NIR spectroscopy method. Although the flotation method is very sensitive at the FDA action level, this technique is time consuming (almost 2 h/sample) and expensive. Although NIR spectroscopy currently lacks the sensitivity of the flotation method, it is rapid, does not require sample preparation, and could be easily automated for a more sophisticated sampling protocol for large flour bulks. Therefore, this method should be reexamined in the future because NIR spectroscopy technology is rapidly improving.

Chronological age-grading of three stored-product beetles by using near-infrared spectroscopy.

J. Perez-Mendoza, J.E. Throne, F.E. Dowell, and J.E. Baker.

The rice weevil (*Sitophilus oryzae* L.), the lesser grain borer (*Rhyzopertha dominica* F.), and the red flour beetle (*Tribolium castaneum* Herbst) are three of the most important pests of stored grain and processed grain products in the U.S. Successful management of these pests requires thorough sampling protocols and subsequent decision-making based on predictive population models or expert system analysis. Because oviposition by these species is not temporally uniform, the accuracy of predictive models used to manage these species can be improved significantly if the age-structure of the pest population is incorporated. However, except for *S. oryzae*, no information on methods to determine the chronological or physiological age of these Coleopterans is known. We previously showed that NIR spectroscopy, a rapid procedure, can be used to determine chronological age of the house fly, a relatively short-lived Dipteran. The objectives of this study were to determine if NIR spectroscopy could be used for determination of chronological age in these three long-lived species of beetles, to determine the role of cuticular lipids in the ability of NIR spectroscopy to age-grade adult *S. oryzae*, and to determine whether water content in adult weevils varies with age and if NIR wavelengths that are absorbed by water have any effect on the ability to determine age. When life spans are normalized on a scale from 0 to 1, the confidence limits on predicted ages for unsexed adults of each species were about ± 0.3 . Thus, younger adults within the first one-third of their life can be easily differentiated from older adults. Based on beta coefficients, absorbance regions corresponding to CH₃, CH₂, and CH groups were the most important for NIR spectroscopy age-grading in the three species. These methyl groups are common constituents of most insect cuticular and internal lipids. Our results provide evidence that these compounds have a significant role in NIR absorption and NIR age classification. Excluding wavelengths associated with H₂O absorbance reduced the percentage of correct age classification.

Determining vitreousness of durum wheat using transmitted and reflected images.

N. Wang, N. Zhang, F. E. Dowell, and T. Pearson.

Durum wheat production accounts for approximately 8 % of the wheat production worldwide and is mainly used to make semolina for macaroni, spaghetti, and other pasta products. The best durum wheat for pasta products should appear hard, glassy and translucent, and have excellent amber color, good cooking quality, and high protein content. Nonvitreous (starchy) kernels are opaque and softer, and result in decreased yield of coarse semolina. Thus, vitreousness of durum wheat has been used as one of the major quality attributes in grading. Traditionally, grain grading has been primarily done by visual inspection of trained personnel. This method is subjective, tedious, and also produces great variations in inspection results between inspectors. The objective of this research was to examine the use of digital imaging technology for determining durum vitreousness. Results showed that 100 % of nonvitreous kernels and 92.6 % of mottled kernels, which is one of the hardest defect categories to consistently detect visually, could be correctly classed. Results of the study also indicated that using transmitted illumination may greatly reduce the hardware and software requirements for the inspection system while providing faster and more accurate results for inspection of vitreousness of durum wheat.

The effectiveness of a high-pressure, water-fogging system in controlling dust emissions at grain receiving.

D.L. Brabec, R.G. Maghirang, and M.E. Casada.

Grain dust at the receiving area is a fire hazard, a health concern, and a sanitation problem and should be controlled. The effectiveness of a high-pressure, water-fogging system in controlling grain dust emissions was evaluated with corn and wheat while spouting 2.1 m³ (60 bu) of grain into a test chamber. Dust/fog emissions and deposits along with entrained airflows were measured for four fog treatments, a control, and an air-blower treatment, each at two grain flow rates. The uncontrolled dust emissions varied with grain type and grain-flow rate. Water-fog sprays, when applied across the top of the test chamber, redirected the airflow downstream of the spray nozzles, and reduced dust emissions significantly. Dust reductions ranged from 60 % to 84 % for corn and 35 % to 73 % for wheat. However, the sprays produced significant fog emissions and deposits in proportion to the liquid supply. At the highest spray-fog rate (855 g/min), fog emission was 32 g/min (3.8 %), and fog deposits ranged from 1.4 to 7.1 mg/cm²/min.

Handling effects on commingling and residual grain in an elevator.

M.E. Ingles, M.E. Casada, and R.G. Maghirang.

Fundamental data are needed that identify and quantify where commingling occurs during identity preserved grain handling at grain elevators so that grains with special desirable characteristics can be kept at a desirable level of purity. This study measured the level of commingling and the weight of residual grain left in equipment when receiving two different colors of corn at the research elevator facility of the USDA–ARS, Grain Marketing and Production Research Center (GMPRC), Manhattan, Kansas. In these tests only the first 15 bu of grain (approximately 1 % of the leg rate per hour) were commingled at greater than a one-percent level. Only the first 40 bu of grain (approximately 2 % of the leg rate per hour) were contaminated at greater than a half-percent level. In a standard operation with a small truckload (300 bu) of corn, the total commingling after the receiving pit and elevator boot amounted to 0.18 % while commingling percentages with weighing scale, grain cleaner and grain scalper were 0.22 %, 0.24 %, and 0.01 %, respectively. This information is needed by elevator operators to better segregate grain with desirable characteristics into separate channels for delivery to end-users. The information is also useful to grain processors for improving their handling of specialty grains.

A novel approach for analyzing grain facility heat treatment data.

H. Akdogan, M. Casada, A. Dowdy, and B. Subramanyam.

This research investigated the use and effectiveness of high temperature for control of stored-product insects in a grain processing facility. Two different heating methods were compared. One method of heating used gas heaters that were placed outside the building. Hot air was channeled inside the building with ducts. The other method used portable electric heaters placed within the building. For both methods, it was important to keep the heat throughout the building as well-mixed as possible, with treatment temperature in the 50–60°C range to kill stored-product insects. A simple mathematical equation was used to describe the percent floor surface area of the facility that was under 50°C as a function of treatment duration. The same equation was successfully used to correlate maximum floor temperature to percent floor surface area. Maps of maximum floor temperatures of the floor surface were created. These computer-generated maps were useful for determining under- and overheated areas of the heat-treated facility. Under-heated areas carry high risk of insect survival and overheated areas pose risk of damaging heat-sensitive equipment. The electric heating in this study resulted in more under-heated areas than gas heating system, whereas gas heating was slower to reach to the target temperature of 50°C.

Books published.

Wheat Gluten Protein Analysis (Edited by P.R. Shewry and G.L. Lookhart). This 198-page book was published by the AACC Eagan Press, St. Paul, MN. The analysis of wheat gluten proteins has a long and distinguished history, extending

over a period exceeding 250 years, reflecting the status of wheat as one of the three major cereal crops that dominate world agriculture (the others being maize and rice) and in particular, its preëminent position as raw material for food processing. The wide use in the food industry depends mainly on the properties of the gluten proteins. These confer viscoelastic properties of doughs, which are exploited in the production of a range of foods including bread, other baked goods, pasta, and noodles. A massive amount of literature has developed on the analysis and properties of wheat gluten proteins, with a particular emphasis on explaining the differences in the functional (i.e. processing) properties that occur between cultivars in terms of variation in the amounts, properties, and interactions of individual gluten protein components. Because gluten proteins have unusual properties, being soluble in alcohol/water mixtures and often present as high molecular mass polymers, much of this literature is published in specialist journals and can be confusing to the nonexpert. The present volume aims to provide standard protocols for the extraction and analysis of wheat gluten proteins based on methods that have been tried and tested in the authors' laboratories. Extensive practical details and tips are provided, as well as suggestions for modifications and examples of applications. We hope that it will prove of value to established cereal chemists as well as those just entering the exciting field of wheat protein chemistry.

Proceeding of the Second International Wheat Quality Conference (Edited by O.K. Chung and J.L. Steele). This 509-page, soft-covered book of the Second International Wheat Quality Conference (IWQC-II) was published by the Grain Industry Alliance (GIA), Manhattan, KS. Following the success of the first International Wheat Quality Conference in 1997 and also held in Manhattan and sponsored by Manhattan's wheat research triad; the American Institute of Baking, Kansas State University, and USDA-ARS Grain Marketing and Production Research Center, the IWQC-I was held 20-24 May, 2001, and featured an excellent group of world-renowned speakers and more than 250 scientists throughout the world from 37 countries attended. The conference was sponsored by the GIA (Dr. Ron Madl, President) and endorsed by the American Association of Cereal Chemists (AACC), the American Society of Agricultural Engineers (ASAE), and the International Association for Cereal Science and Technology (ICC). The ICC, headquarters in Vienna, Austria, held its Executive Committee Meeting in Manhattan prior to IWQC-II and was the first ICC event held in the U.S. since its founding in 1955, because Dr. Okkyung Kim Chung, the conference co-chair, was president of ICC.

The topics include issues and concerns of end users, wheat breeding and biotechnology, quality assessment methods, food safety, international quality standards and marketing procedures, economics of wheat trade in the world, and advances in wheat processing technology. Each session was one-half day long, with a one-hour discussion at the end of the session. Discussion sessions were led by experts from Australia, Belgium, Canada, France, Germany, Hong Kong, Mexico, the Netherlands, Russia, Switzerland, the United Kingdom, and the U.S. The proceedings contained full-length papers of invited speakers of each technical session and 80 abstracts of the papers presented at the poster session.

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MINNESOTA

CEREAL DISEASE LABORATORY, USDA—ARS

University of Minnesota, 1551 Lindig St., St. Paul, MN 55108, USA.

www.cdl.umn.edu

D.L. Long, J.A. Kolmer, Y. Jin, M.E. Hughes, and L.A. Wanschura.

Wheat Rusts in the United States in 2003.

Wheat stem rust. The first reports of wheat stem rust in 2003 were in mid-April, when trace amounts were found in a plot of the susceptible cultivar McNair 701 in southern Texas at Uvalde. By late April, wheat stem rust was severe in plots of McNair 701 and Chinese Spring at Uvalde. In mid-May, late developing tillers provided good niches for the stem rust to develop in southern Texas. During late May, traces of stem rust were found in a plot of the susceptible cultivar McNair 701 in north central Oklahoma. In late May, stem rust was found in late maturing lines in the nursery at Baton Rouge, LA. Wheat stem rust was very light throughout the southern U.S. in 2003.

By mid-July, traces of wheat stem rust were observed on the susceptible spring wheat cultivar Baart in south central Minnesota plots. In late July, trace–20 % stem rust severities were observed on Baart and Max in southeastern North Dakota. Trace–30 % severities were observed on Baart in northwestern and north central Minnesota. Up to 30 % severities were observed on the winter wheat cultivar Norstar in northeastern North Dakota. The incidence of wheat stem rust infections was lighter than normal in the northern Great Plains this year, because little wheat stem rust developed in the southern and central U.S. All of the current spring wheat cultivars and most of the winter wheat cultivars are resistant to the current stem rust race population.

Wheat stem rust race virulence. Race QFCS was the most common stem rust race identified from collections made in the U.S. in 2003 (Table 1). Although this race was frequently found in surveys in previous years, it has become the predominant race on susceptible wheat, barley, and wild barley (*Hordeum jubatum*) in 2003. Race QFCS has virulence on *Sr5*, *8a*, *9a*, *9d*, *9g*, *10*, *17*, and *21*. Several HRWW and soft wheats were found to be susceptible to QFCS based on seedling tests, including Thunderbolt, Onaga, Ankor, Nuf Frontier, Lakin, Truman, Roane, and Additions. However, the majority of wheat cultivars grown in the United States are resistant to race QFCS.

Wheat leaf rust. Southern Plains. In mid-February, light amounts of leaf rust were found on wheat in the central and Rolling Plains areas of Texas. The most severe rust was on the cultivar Jagger. In early March, wheat leaf rust development was slowed in central Texas plots, because of the cool temperatures in late February. The most severe rust was in border rows of TAM 110 where 10–20 % severities were observed on the lower leaves. In early-April, leaf rust infections were light in wheat fields and were at high levels on susceptible cultivars in nursery plots in southern and central Texas. In the last week of March in southern and central Texas, leaf rust severities up to 60 % were on the lower leaves of cultivars in breeding nurseries and trace–10 % severity levels were on the lower

Table 1. Races of *Puccinia graminis* f. sp. *tritici* identified from wheat in 2003. Pgt race code after Roelfs and Martens (*Phytopathology* 78:526-533). Set four consists of *Sr9a*, *Sr9d*, *Sr10*, and *SrTmp*.

State	Source	Collections	Isolates	Percentage of isolates of Pgt– race		
				QCCJ	QFCS	RCCF
MN	Field	1	3		100	
MN	Nursery	5	9	33	67	
ND	Nursery	11	25		96	4
OK	Nursery	1	3		100	
SD	Nursery	1	5		100	
TX	Nursery	1	10		100	
U.S.	Field	1	3		100	
	Nursery	20	52	6		92
	Total	20	55	5		93

leaves in fields. The dry and cool weather in late March and early April contributed to the slow leaf rust development in the southern U.S.

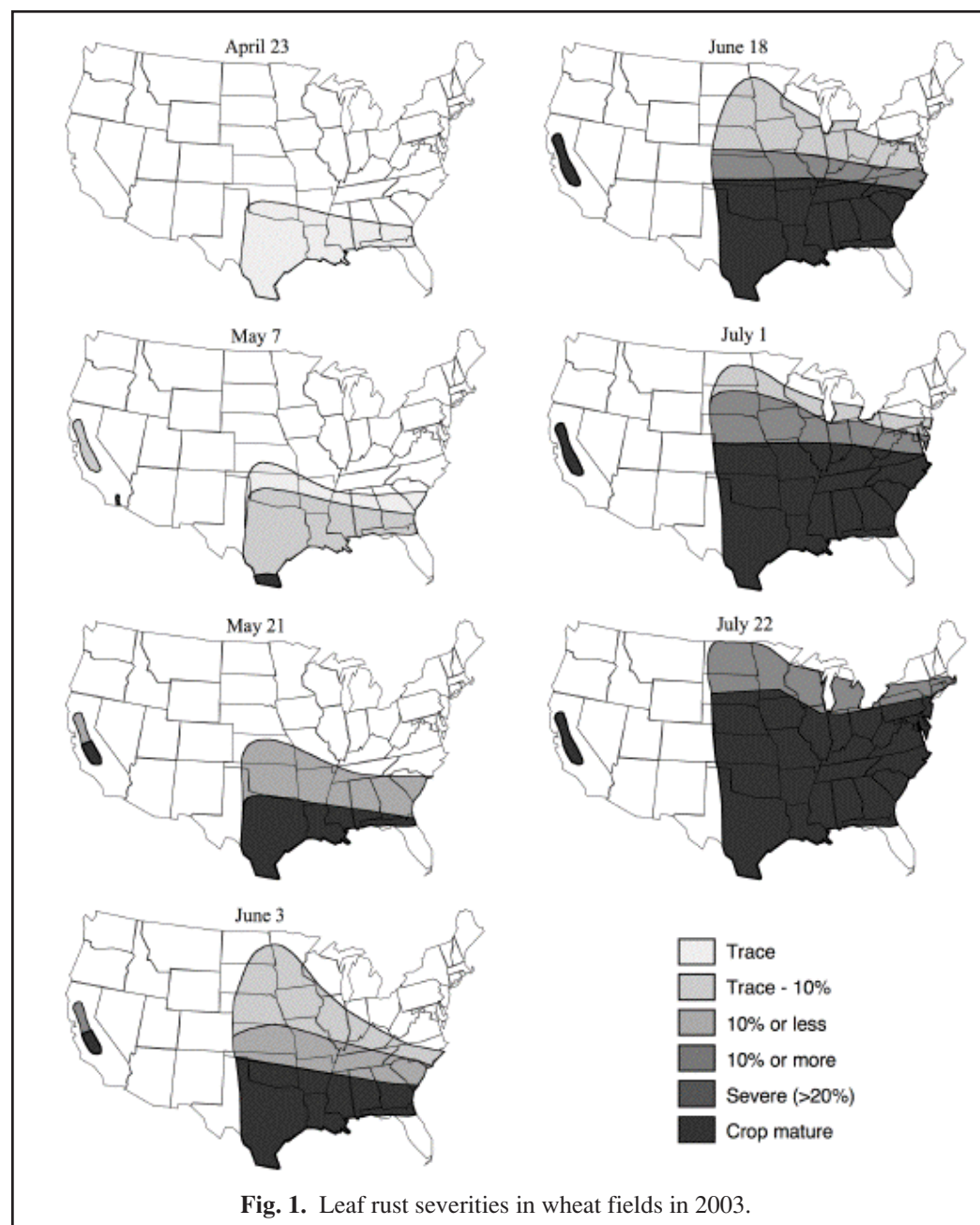


Fig. 1. Leaf rust severities in wheat fields in 2003.

In mid-April, even with the dry conditions, leaf rust was increasing throughout Texas, but overall rust severities were lighter than normal for this time of the year (Fig. 1). In a central Texas nursery on the susceptible cultivar Jagger, the leaves were completely dead because of the rust. In mid-April, leaf rust was increasing in southern Oklahoma on susceptible cultivars. In early May, susceptible cultivars in central Texas had moderate to light infections, whereas in northern Texas wheat at the late flower to early dough growth stages did not have any leaf rust infection. In early May, traces of leaf rust were found in plots of susceptible cultivars in southwestern Oklahoma. Leaf rust in Oklahoma developed when the crop was at the dough growth stage, which resulted in little loss

due to leaf rust. Infection sites in the southern winter wheat provided inoculum for the northern wheat area.

Central Plains. In early May, wheat leaf rust was found in light amounts in south central Kansas fields. By the third week in May, severity levels as high as 10 % were observed on flag leaves in a few fields of Jagger. During the last week in May, leaf rust was severe in plots and fields of susceptible cultivars from central Kansas to west central Missouri (Fig. 1). In fields of Jagger at the late berry stage in south central Kansas, 60 % severities were found on flag leaves. In fields of Jagger in northeast Kansas, 10 % severities were observed on flag leaves. In central Kansas varietal plots, rust severities ranged from trace to 60 %. Throughout Kansas and Missouri wheat leaf rust and stripe rust were competing on many cultivars for the same leaf tissue. Usually stripe rust increases faster because it can develop earlier and increase faster at cooler temperatures than leaf rust. In southern Kansas, losses due to leaf rust were severe in cultivars like

Jagger but in other leaf rust susceptible cultivars losses were light (Table 4, p. 243). During late May, 20 % leaf rust severities were observed on *Ae. cylindrica* (goatgrass) growing in the roadside in south central Kansas.

In the second week in June in eastern Nebraska, low to moderate leaf rust severities were found in fields and plots. Drought-like conditions in areas like western Nebraska slowed leaf rust development.

Northern Plains. In late May, traces of wheat leaf rust were found in winter wheat plots in east central Minnesota. On 28 May, traces of wheat leaf rust were observed in spring wheat fields in south central and eastern North Dakota. In mid-June, low levels of leaf rust infections were observed on the flag leaves of HRWW at anthesis in an east central South Dakota nursery. In early June, leaf rust also was found in spring wheat cultivars in the South Dakota nursery.

During the second week in June, leaf rust infections were found in winter and spring wheat fields in the southeast and south central part of North Dakota. Leaf rust severities in the fields ranged from 1 to 25 %, with most fields at low severity levels. Warm temperatures and high humidity favored leaf rust development. In the third week in June, trace–10 % leaf rust severities were observed at anthesis in susceptible winter wheat plots in east central Minnesota. Infections were mostly on flag-1 and flag-2 leaves. In the final week in June, susceptible winter wheat cultivars from east central Minnesota to west central South Dakota had 60 % rust severities. Susceptible cultivars like Jagger and Expedition, had severities of 60 %, but most cultivars had only trace levels of infection on the flag leaves. The rust infections in South Dakota and Minnesota probably originated from inoculum sources in Texas, Oklahoma, and Kansas.

In the last week of June, susceptible spring wheat cultivars in southern Minnesota plots had 20 % rust severities, with most infections on the lower leaves. Traces of leaf rust were observed in many of the spring wheat fields in southern Minnesota. In mid-July, 20–40 % wheat leaf rust severities were observed on flag leaves of spring wheat cultivars in fields from southeastern North Dakota, northwestern South Dakota, to southwestern Minnesota. Many wheat fields were sprayed with fungicide which prevented losses due to rust.

In late July, trace–60 % leaf rust severities were observed in spring wheat varietal plots in central and eastern North Dakota plots. In farm fields in central and southeastern North Dakota severity levels of up to 40 % were observed on the commonly grown wheat cultivars. In the northern tier of counties in North Dakota leaf rust was at reduced levels because the crop maturity was later than normal. Many wheat fields in the Red River Valley of the north were sprayed with fungicide to reduce loss due to foliar diseases.

This year leaf rust was severe and concentrated in the upper Midwest. Rust inoculum arrived from the south in late May and early June with rain showers and temperature and moisture conditions were good for infection and spread of leaf rust. The spring wheat cultivars currently grown have less effective resistance to leaf rust than those that were popular 10–15 years ago. Losses to wheat leaf rust occurred in the most susceptible cultivars (Table 5, p. 235).

Southeast. In late March, wheat leaf rust was light in plots in the southern SRWW area from Georgia to Louisiana. In mid-April, from central Louisiana to Georgia, light amounts of leaf rust were observed in research plots and fields. In early May, the highest leaf rust severities (60 %) were in plots of susceptible cultivars in central Louisiana and southwestern Georgia. Only trace levels of leaf rust were found in southeastern Arkansas wheat plots. In early May, leaf rust severities of 30 % were reported in susceptible wheat plots in Louisiana and severities of 60–70 % were reported in plots in south central Georgia. Wheat leaf rust was lighter and developed later than normal throughout the southern SRWW area and did not cause much yield loss. In late May in eastern Arkansas, leaf rust had developed late on several cultivars including CK9663 that had been previously highly resistant. Stripe rust developed first in this area reducing the development of leaf rust.

Mideast. During the second week in June, trace–10 % leaf rust severities were reported in plots, and traces in fields of soft red winter wheat cultivars from northeastern Missouri to northwestern Ohio. Leaf rust infections were reduced due to cooler than normal temperatures in the region and the presence of wheat stripe rust.

East. In early June, leaf rust severities ranged from trace to 15 % on susceptible cultivars in a nursery on the eastern shore of Virginia. In mid-June, a plot of the cultivar Massey in northwestern Virginia had leaf rust severity of 80 %. Wheat leaf rust was lighter than normal in the eastern U.S. this year.

California. In many areas of California in early May, wheat leaf rust was difficult to find because of the cool weather and abundance of stripe rust. However, leaf rust was severe in commercial fields in the Imperial Valley. Fields of the

Table 2. Races of *Puccinia triticina* in the U.S. in 2003 determined by virulence to 16 near-isogenic lines of Thatcher wheat with leaf rust-resistance genes. Area 1 includes the U.S. states of AL, AR, FL, GA, LA, MS, NC, and SC; Area 2, DE, MD, NJ, NY, PA, VA, and WV; Area 3, IL, IN, KY, MI, MO, OH, TN, and WI; Area 4, NM, OK, and TX; Area 5, CO, IA, KS, and NE; Area 6, MN, MT, ND, SD, and WY; Area 7, CA, and UT; and Area 8, ID, OR, and WA (see Fig. 4).

Race	Virulence combination (ineffective <i>Lr</i> genes)	Area 1		Area 2		Area 3		Area 4		Area 5		Area 6		Area 7		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBD	14a	0	0	1	10.0	0	0	0	0	0	0	0	0	1	3.4	2	0.3
BBBG	10	0	0	0	0	0	0	0	0	0	0	6	2.2	0	0	6	1.0
CBMT	3,3ka,30,B,10,14a,18	3	5.4	0	0	0	0	0	0	0	0	0	0	0	0	3	0.5
KBBG	2a,2c,3,10	1	1.8	0	0	0	0	0	0	3	4.1	16	5.9	0	0	20	3.4
KBBJ	2a,2c,3,10,14a	0	0	0	0	1	5.6	0	0	1	1.4	7	2.6	0	0	9	1.6
KCBJ	2a,2c,3,26,10,14a	0	0	0	0	0	0	0	0	1	1.4	3	1.1	0	0	4	0.7
KFBJ	2a,2c,3,24,26,10,14a	0	0	0	0	0	0	1	0.8	0	0	2	0.7	0	0	3	0.5
KGBG	2a,2c,3,16,10	0	0	0	0	0	0	0	0	0	0	10	3.7	2	6.9	12	2.1
MBBJ	1,3,10,14a	0	0	0	0	0	0	0	0	1	1.4	0	0	4	13.8	5	0.9
MBBK	1,3,10,14a,18	0	0	0	0	0	0	0	0	0	0	0	0	2	6.9	2	0.3
MBDS	1,3,17,B,10,14a	8	14.3	0	0	10	55.6	37	30.3	18	24.7	28	10.4	8	27.6	109	18.8
MBGJ	1,3,11,10,14a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.2
MBRJ	1,3,3ka,11,30,10,14a	2	3.6	0	0	0	0	5	4.1	1	1.4	1	0.4	0	0	9	1.6
MBRK	1,3,3ka,11,30,10,14a,18	4	7.1	0	0	0	0	2	1.6	0	0	0	0	0	0	6	1.0
MBRK	1,3,3ka,11,30,B,10,14a,18	1	1.8	0	0	0	0	0	0	0	0	0	0	0	0	1	0.2
MCBJ	1,3,26,10,14a	0	0	0	0	1	5.6	1	0.8	0	0	0	0	0	0	2	0.3
MCDS	1,3,26,17,B,10,14a	11	19.6	0	0	2	11.1	12	9.8	13	17.8	19	7.0	9	31.0	67	11.6
MCJS	1,3,26,11,17,B,10,14a	0	0	6	60.0	0	0	0	0	0	0	0	0	0	0	6	1.0
MCRJ	1,3,26,3ka,11,30,10,14a	0	0	0	0	0	0	2	1.6	0	0	0	0	0	0	2	0.3
MCRK	1,3,26,3ka,11,30,10,14a,18	6	10.7	0	0	0	0	0	0	0	0	2	0.7	0	0	8	1.4
MDBJ	1,3,24,10,14a	2	3.6	0	0	0	0	3	2.5	0	0	0	0	0	0	5	0.9
MDRJ	1,3,24,3ka,11,30,10,14a	0	0	0	0	0	0	4	3.3	0	0	0	0	0	0	4	0.7
MJBj	1,3,16,24,10,14a	0	0	0	0	0	0	0	0	1	1.4	1	0.4	0	0	2	0.3
NBBK	1,2c,10,14a,18	0	0	0	0	0	0	0	0	0	0	1	0.4	0	0	1	0.2
SBDB	1,2a,2c,17	0	0	0	0	0	0	0	0	2	2.7	0	0	0	0	2	0.3
SBDD	1,2a,2c,17,14a	0	0	0	0	0	0	0	0	3	4.1	0	0	0	0	3	0.5
SBDJ	1,2a,2c,17,10,14a	0	0	0	0	0	0	3	2.5	1	1.4	0	0	0	0	4	0.7
TBBD	1,2a,2c,3,14a	0	0	0	0	0	0	0	0	1	1.4	0	0	0	0	1	0.2
TBBJ	1,2a,2c,3,10,14a	0	0	0	0	0	0	2	1.6	6	8.2	48	17.8	0	0	56	9.7
TBBS	1,2a,2c,3,B,10,14a	0	0	0	0	0	0	0	0	0	0	8	3.0	0	0	8	1.4
TBDF	1,2a,2c,3,17,14a,18	0	0	0	0	0	0	0	0	0	0	2	0.7	0	0	2	0.3
TBDS	1,2a,2c,3,17,B,10,14a	0	0	0	0	4	22.2	8	6.6	6	8.2	19	7.0	0	0	37	6.4
TCBJ	1,2a,2c,3,26,10,14a	1	1.8	0	0	0	0	0	0	2	2.7	0	0	0	0	3	0.5
TCDS	1,2a,2c,3,26,17,B,10,14a	1	1.8	0	0	0	0	6	4.9	4	5.5	10	3.7	0	0	21	3.6
TCTD	1,2a,2c,3,26,3ka,11,17,30,14a	0	0	2	20.0	0	0	0	0	0	0	0	0	0	0	2	0.3
TDBJ	1,2a,2c,3,24,10,14a	1	1.8	0	0	0	0	1	0.8	2	2.7	2	0.7	0	0	6	1.0
TFBG	1,2a,2c,3,24,26,10	0	0	0	0	0	0	0	0	0	0	4	1.5	0	0	4	0.7
TFBJ	1,2a,2c,3,24,26,10,14a	2	3.6	0	0	0	0	4	3.3	3	4.1	1	0.4	2	6.9	12	2.1
TGBJ	1,2a,2c,3,16,10,14a	0	0	0	0	0	0	0	0	1	1.4	7	2.6	0	0	8	1.4
TGDS	1,2a,2c,3,16,17,B,10,14a	0	0	0	0	0	0	1	0.8	0	0	7	2.6	0	0	8	1.4
THBJ	1,2a,2c,3,16,26,10,14a	0	0	0	0	0	0	10	8.2	2	2.7	56	20.7	0	0	68	11.7
THMJ	1,2a,2c,3,16,26,3ka,30,10,14a	0	0	0	0	0	0	1	0.8	0	0	1	0.4	0	0	2	0.3
TLGJ	1,2a,2c,3,9,11,10,14a	13	23.2	0	0	0	0	2	1.6	0	0	0	0	0	0	15	2.6
TLGK	1,2a,2c,3,9,11,10,14a,18	0	0	1	10.0	0	0	0	0	0	0	0	0	0	0	1	0.2
TNBJ	1,2a,2c,3,9,24,10,14a	0	0	0	0	0	0	3	2.5	0	0	0	0	0	0	3	0.5
TNRJ	1,2a,2c,3,9,24,3ka,11,30,10,14a	0	0	0	0	0	0	14	11.5	1	1.4	9	3.3	1	3.4	25	4.3
Total		56		10		18		122		73		270		29		580	

durum wheat cultivar Orita, at the soft dough stage, had 70–80 % leaf rust severities in early May. By mid-late May, wheat leaf rust was severe (50–80 % severity) on susceptible cultivars in yield trials and fields in the Central Valley of California. High levels were detected on the few susceptible cultivars that were not affected by stripe rust. No leaf rust

was detected on durum wheat in the Central Valley. In late July, 40 % rust severities were observed in wheat growing in plots at Tulalake in northern California.

Table 3. Virulence frequencies (%) of *Puccinia triticina* in the U.S. in 2003 to 16 differential lines of Thatcher wheat with leaf rust resistance genes. Area 1 includes the U.S. states of AL, AR, FL, GA, LA, MS, NC, and SC; Area 2, DE, MD, NJ, NY, PA, VA, and WV; Area 3, IL, IN, KY, MI, MO, OH, TN, and WI; Area 4, NM, OK, and TX; Area 5, CO, IA, KS, and NE; Area 6, MN, MT, ND, SD, and WY; Area 7, CA, and UT; and Area 8, ID, OR, and WA (see Fig. 2).

Resistance gene	Area 1		Area 2		Area 3		Area 4		Area 5		Area 6		Area 7		U.S. Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
<i>Lr1</i>	52	92.9	9	90.0	17	94.4	121	99.2	68	93.2	226	83.7	26	89.7	521	89.8
<i>Lr2a</i>	19	33.9	3	30.0	5	27.8	56	45.9	39	53.4	212	78.5	52	17.2	339	58.4
<i>Lr2c</i>	19	33.9	3	30.0	5	27.8	56	45.9	39	53.4	213	78.9	5	17.2	340	58.6
<i>Lr3</i>	56	100.0	9	90.0	18	100.0	119	97.5	67	91.8	263	97.4	28	96.6	562	96.9
<i>Lr9</i>	13	23.2	1	10.0	0	0	19	15.6	1	1.4	9	3.3	1	3.4	44	7.6
<i>Lr16</i>	0	0	0	0	0	0	12	9.8	4	5.5	82	30.4	2	6.9	100	17.2
<i>Lr24</i>	5	8.9	0	0	0	0	30	24.6	7	9.6	19	7.0	3	10.3	64	11.0
<i>Lr26</i>	21	37.5	8	80.0	3	16.7	37	30.3	25	34.2	98	36.3	11	37.9	204	35.2
<i>Lr3ka</i>	16	28.6	2	20.0	0	0	28	23.0	2	2.7	13	4.8	1	3.4	62	10.7
<i>Lr11</i>	26	46.4	9	90.0	0	0	29	23.8	2	2.7	12	4.4	1	3.4	80	13.8
<i>Lr17</i>	20	35.7	8	80.0	16	88.9	67	54.9	47	64.4	85	31.5	17	58.6	261	45.0
<i>Lr30</i>	16	28.6	2	20.0	0	0	28	23.0	2	2.7	13	4.8	1	3.4	62	10.7
<i>LrB</i>	24	42.9	6	60.0	16	88.9	64	52.5	41	56.2	91	33.7	17	58.6	260	44.8
<i>Lr10</i>	56	100.0	7	70.0	18	100.0	122	100.0	67	91.8	268	99.3	28	96.6	568	97.9
<i>Lr14a</i>	55	98.2	10	100.0	18	100.0	122	100.0	68	93.2	234	86.7	27	93.1	536	92.4
<i>Lr18</i>	14	25.0	1	10.0	0	0	2	1.6	0	0	5	1.9	2	6.9	24	4.1
Total	56		10		18		122		73		270		29		580	

Wheat Leaf Rust Virulence. The 2003 leaf rust race identifications from the most common races identified are presented in Tables 2 (p. 241) and 3. A total of 46 leaf rust races were found in the U.S. in 2003. From the central and southern Plains the most common races were M-B- (virulent to *Lr1*, *Lr3*, *Lr10*, *Lr17*, +) (Table 3). Many of the MBDS and MCDS races were identified from collections made from Jagger, which is widely grown in the southern and central Plains states. There has been an increase in T-races (TBBJ, TBDS, and THBJ) in the northern wheat-growing area. Many of the T-races with virulence to *Lr2a* and *Lr16* were identified from rust collections made from northern hard spring wheats. There also has been an increase in the number of T-races (TNRJ and TNBJ) with virulence to *Lr9*, *Lr10*, and *Lr24* in Texas. Many of the T-races with virulence to *Lr9* and *Lr24* were identified from collections made from the cultivars Lockett (*Lr9* resistance) and Thunderbolt (*Lr41* resistance).

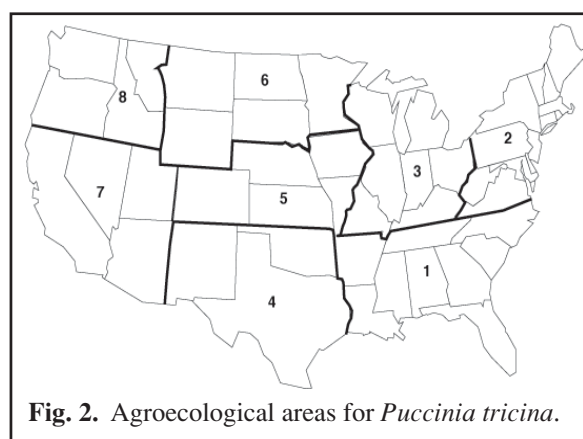


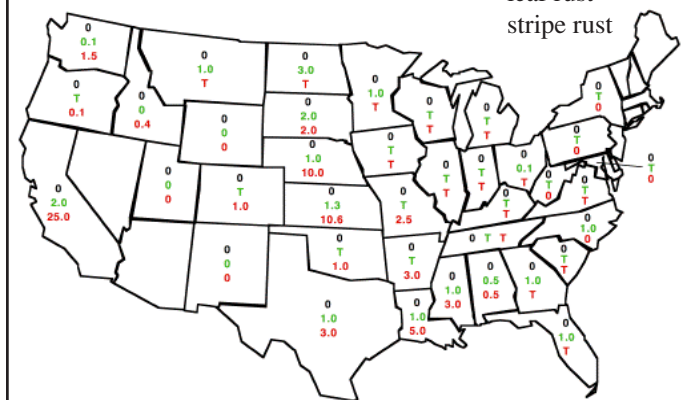
Fig. 2. Agroecological areas for *Puccinia triticina*.

Yield loss estimates due to leaf rust are in Table 4 (p. 243), Fig. 3 (winter wheat, p. 244), and Table 5 (spring and durum wheat, p. 245).

Wheat stripe rust. Southern Plains. In mid-February, many hot spots of stripe rust infection (1–3 feet in circumference) were found in central Texas wheat plots, suggesting stripe rust might have overwintered in this region. In a field 70 miles east of San Antonio, stripe rust was present in a commercial field of Ogallala and in the nursery plots severities

Table 4. Estimated losses in winter wheat due to rust in 2003 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to					
				Stem rust		Leaf rust		Stripe rust	
				Percent	1,000 bushels	Percent	1,000 bushels	Percent	1,000 bushels
AL	75	42.0	3,150	0.0	0.0	0.5	15.9	0.5	15.9
AR	570	50.0	28,500	0.0	0.0	T*	T	3.0	881.4
CA	370	61.0	22,570	0.0	0.0	2.0	618.4	25.0	7,729.5
CO	2,200	35.0	77,000	0.0	0.0	T	T	1.0	777.8
DE	47	41.0	1,927	0.0	0.0	0.0	0.0	0.0	0.0
FL	12	41.0	492	0.0	0.0	1.0	5.0	T	T
GA	230	46.0	10,580	0.0	0.0	1.0	106.9	T	T
ID	720	80.0	57,600	0.0	0.0	0.0	0.0	0.4	231.3
IL	810	65.0	52,650	0.0	0.0	T	T	T	T
IN	430	69.0	29,670	0.0	0.0	T	T	T	T
IA	19	61.0	1,159	0.0	0.0	T	T	T	T
KS	10,000	48.0	480,000	0.0	0.0	1.3	7,082.9	10.6	57,752.6
KY	330	62.0	20,460	0.0	0.0	T	T	T	T
LA	140	41.0	5,740	0.0	0.0	1.0	61.1	5.0	305.3
MD	145	37.0	5,365	0.0	0.0	T	T	0.0	0.0
MI	660	68.0	44,880	0.0	0.0	T	T	T	T
MN	23	42.0	966	0.0	0.0	1.0	9.8	T	T
MS	125	49.0	6,125	0.0	0.0	1.0	63.8	3.0	191.4
MO	870	61.0	53,070	0.0	0.0	T	T	2.5	1,360.8
MT	1,720	37.0	63,640	0.0	0.0	1.0	642.8	T	T
NE	1,820	46.0	83,720	0.0	0.0	1.0	940.7	10.0	9,406.7
NJ	26	42.0	1,092	0.0	0.0	0.0	0.0	0.0	0.0
NM	140	30.0	4,200	0.0	0.0	0.0	0.0	0.0	0.0
NY	120	53.0	6,360	0.0	0.0	T	T	0.0	0.0
NC	410	36.0	14,760	0.0	0.0	1.0	149.1	0.0	0.0
ND	120	49.0	5,880	0.0	0.0	3.0	181.9	T	T
OH	1,000	68.0	68,000	0.0	0.0	0.1	68.1	T	T
OK	4,600	39.0	179,400	0.0	0.0	T	T	1.0	1,812.1
OR	940	51.0	47,940	0.0	0.0	T	T	0.1	48.0
PA	165	43.0	7,095	0.0	0.0	T	T	0.0	0.0
SC	185	39.0	7,215	0.0	0.0	T	T	T	T
SD	1,380	43.0	59,340	0.0	0.0	2.0	1,236.3	2.0	1,236.3
TN	270	50.0	13,500	0.0	0.0	T	T	T	T
TX	3,450	28.0	96,600	0.0	0.0	1.0	1006.3	3.0	3,018.8
UT	125	41.0	5,125	0.0	0.0	0.0	0.0	0.0	0.0
VA	160	46.0	7,360	0.0	0.0	T	T	T	T
WA	1,800	65.0	117,000	0.0	0.0	0.1	118.9	1.5	1,783.5
WV	7	41.0	287	0.0	0.0	T	T	0.0	0.0
WI	175	69.0	12,075	0.0	0.0	T	T	T	T
WY	145	27.0	3,915	0.0	0.0	0.0	0.0	0.0	0.0
Total	36,534	46.7	1,706,408		0.0		12,308.1		86,551.4
U.S. % loss				0.03		0.68		4.79	
U.S. Total	36,541	46.7	1,707,069						

Fig. 3. 2003 winter wheat loss (%) to rust:stem rust
leaf rust
stripe rust

were high on Ogallala and Coronado. In late February, cold temperatures in central Texas slowed stripe rust in plots, but conditions were still good for stripe rust to increase since there was regular precipitation in late February and early March. By early March, stripe rust had spread throughout the central Texas nurseries. In early April, wheat stripe rust severities were high in wheat fields in southern and central Texas (Fig 4). Stripe rust infections were high in several thousand acres of Coronado in central Texas. In mid-March, plants in a few fields of Coronado died because of stripe rust. Many of the fields in central Texas were sprayed for rust control. Stripe rust development slowed during the later part of March and early April because of dry field conditions. In early April, low levels of stripe rust infection were

found in fields west of Dallas. The wheat cultivars Jagger, Cutter, and Jagelene had the best stripe rust resistance in the Texas nurseries. In mid-April, stripe rust development was slowing in south Texas, but it was still possible to find some

fresh pustules at all locations. In central and north central Texas, stripe rust was severe even though much of the area had been under drought conditions. During the last week in April, wheat stripe rust infections were increasing on susceptible cultivars from central to northern Texas. This was the worst stripe rust epidemic in the last forty years in central Texas.

In 2003, stripe rust overwintering sites occurred in more locations than in previous years throughout the southern U.S. wheat-growing area. Where stripe rust spores are deposited and infect wheat in late autumn and early winter, overwintering sites develop that are very critical to where stripe rust will occur the next year.

In early May, hot spots of stripe rust foci were found in central to north central Oklahoma plots. A wheat field in north central Oklahoma was heavily infected with stripe rust. In early May in southwestern

**Fig. 4.** Stripe rust severities in wheat fields in 2003.

Table 5. Estimated losses in spring wheat due to rust in 2002 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to					
				Stem rust		Leaf rust		Stripe rust	
				Percent	1,000 bushels	Percent	1,000 bushels	Percent	1,000 bushels
CO	24	100.0	2,400	0.0	0.0	0.0	0.0	0.0	0.0
CO	29	40.0	1,160	0.0	0.0	T	T	T	T
ID	450	66.0	29,700	0.0	0.0	0.0	0.0	0.7	209.4
MN	1,800	58.0	104,400	T	T	1.0	1,054.5	T	T
MT	2,700	22.0	59,400	0.0	0.0	T*	T	T	T
NV	4	75.0	300	0.0	0.0	0.0	0.0	0.0	0.0
ND	6,400	39.5	252,800	T	T	1.0	2,553.5	T	T
OR	140	40.0	5,600	0.0	0.0	0.1	5.6	0.3	16.9
SD	1,340	42.0	56,280	0.0	0.0	1.0	568.5	T	T
UT	10	46.0	460	0.0	0.0	0.0	0.0	0.0	0.0
WA	545	41.0	22,345	0.0	0.0	0.1	23.2	3.5	811.3
WI	5	45.0	225	0.0	0.0	T	T	0.0	0.0
WY	6	25.0	150	0.0	0.0	0.0	0.0	0.0	0.0
Total from above									
	13,429	39.7	532,820		T		4,205.3		1,037.6
U.S. % loss				T		0.78		0.19	
U.S. total									
	13,429	39.7	532,820						

Table 6. Estimated losses in durum wheat due to rust in 2002 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to					
				Stem rust		Leaf rust		Stripe rust	
				Percent	1,000 bushels	Percent	1,000 bushels	Percent	1,000 bushels
AZ	115	100.0	11,500	0.0	0.0	0.0	0.0	0.0	0.0
CA	115	100.0	11,500	0.0	0.0	1.0	129.1	10.0	1,292.1
MN	2	58.0	116	0.0	0.0	0.0	0.0	0.0	0.0
MT	630	23.0	14,490	0.0	0.0	0.0	0.0	0.0	0.0
ND	1,980	29.5	58,410	0.0	0.0	0.0	0.0	0.0	0.0
SD	27	23.0	621	0.0	0.0	0.0	0.0	0.0	0.0
Total from above									
	2,869	33.7	96,637			0.0	129.1		1,292.1
U.S. % loss					0.00		0.13		1.32
U.S. Total									
	2,869	33.7	96,637						

Oklahoma, plots of the susceptible cultivars 2137, Above, AP502CL, Custer, Trego, and Intrada had lost their flag leaves because of a combination of stripe rust and moisture stress. Resistant cultivars Jagger, Cutter, Thunderbolt and several advanced lines from Oklahoma, still had green leaves. Cultivars with an intermediate resistance to stripe rust (Ok101, 2174, and 2145) also had green flag leaves. In northern Oklahoma, susceptible cultivars had lost their flag leaves due to the stripe rust and drought. Other cultivars such as Jagger which were resistant to stripe rust did much better in this area. Losses due to stripe rust in Oklahoma will be less than in 2001 because of the drought-like conditions in some areas of the state in May (Table 4, p. 243).

Central Plains. In mid-May, wheat stripe rust was prevalent throughout the entire state of Kansas at varying degrees of severity. The disease was most severe in the southern areas of the state. Cultivars Jagger, Big Dawg, and Betty were resistant. In some areas of Kansas, the more susceptible cultivars such as 2137, AGSECO 7853, Kalvesta, OK101, Stanton, Venango, Oro Blanco, Lakin, Trego, TAM 107, and TAM 110 had high stripe rust severities. A 30–40 % yield loss was estimated for the highly susceptible cultivars.

In late May, stripe rust was severe (60 % infection level) in central and southern Kansas plots and fields (Fig. 2). There was much more stripe rust in Kansas in 2003 than in 2002. In both 2003 and 2002, a cool spring with nighttime temperatures in the 40s and 50s °F plus humid weather were conducive for stripe rust development throughout the Great Plains. However, the rust inoculum load from Texas in 2003 was greater, which caused more rust development. Stripe rust losses were estimated at 10 % in Kansas in 2003 (Table 4, p. 243). Wheat stripe rust development in 2003 in the southern and central Great Plains was comparable to 2001.

In late May, traces of stripe rust were found in plots of susceptible wheat in south central Nebraska. In mid-June, stripe rust was light in most fields in central and eastern Nebraska. During the last week of June, winter wheat fields and plots in western Nebraska had stripe rust severities from trace to 60 %.

Northern Plains. During late May, trace amounts of stripe rust were found at the late jointing growth stage in east central South Dakota winter wheat plots. In the second week of June in east central Minnesota, winter wheat plots had trace levels of stripe rust. A focal point of severe infection was found in a winter wheat plot in St. Paul, indicating that stripe rust may have overwintered in Minnesota or arrived in late April or early May. During the third week of June, 60% severities were observed in susceptible winter wheat plots (e.g., Coker 9835) at the Rosemount Experiment Station in east central Minnesota. In other winter wheat plots severities ranged from 0–40 %.

In early June, wheat stripe rust was found in winter wheat and spring wheat nurseries in eastern South Dakota. In some susceptible winter wheat lines (e.g., Trego) stripe rust severity was 100 %. During the last week in June, winter wheat fields and plots in south central South Dakota had stripe rust severities from trace to 60 %.

On 20 June, winter wheat plots in east central Minnesota had wheat stripe rust severity levels between trace to 60 %. Coker 9835 had severities between 40–60 %. Cultivars with *Lr26/Yr9/Sr31* genes on the wheat-rye T1B-1R translocation also tended to have higher stripe rust severities. Many cultivars had a resistant response characterized by necrotic strips; moderately resistant cultivars had necrotic strips with stripe rust pustules, moderately susceptible cultivars had chlorotic strips with pustules, and susceptible cultivars had strips of pustules without necrosis or chlorosis. Cultivars known to have *Lr34/Yr18* had a moderately resistant response.

In late June, stripe rust infections were found in spring wheat plots in east central Minnesota. Some of the cultivars (e.g. Briggs and Walworth) had stripe rust severities of 10 %. The cooler temperatures with sufficient moisture levels were conducive for stripe rust development in the north central region.

In late June, severe stripe rust was found in spring wheat fields in east central North Dakota. Fields sprayed with fungicides in the eastern North Dakota area were rust free. In mid-July, 40 % stripe rust severities were found on flag leaves in some wheat fields at the early berry stage in southeastern North Dakota. The rust pustules on the leaves were still sporulating, since the nighttime temperatures were less than 60°F in that area. In late July, active stripe rust pustules were observed in wheat varietal plots throughout the state of North Dakota.

Southeast. In early March, stripe rust was increasing on a few cultivars in south central Louisiana. Stripe rust was light but increasing in spots. Weather conditions were ideal for rust infection in early March. In early April, stripe rust infections were increasing throughout plots in southern Louisiana. Many wheat fields in Louisiana were sprayed for stripe rust.

By mid-April, stripe rust was severe in southern Louisiana nurseries, with 80 % severities in susceptible cultivars. Throughout Louisiana, stripe rust was common and many fields were sprayed with fungicides to reduce yield losses. Wheat cultivars Terral LA422 and AGS 2000, which are widely grown in Louisiana, were susceptible to stripe rust. Heavy infections of stripe rust have occurred in four of the last 6 years in Louisiana.

In early April, a focal point of stripe rust infection that had overwintered was found in wheat plots in northwestern Arkansas. In mid-April, stripe rust was increasing in southern and eastern Arkansas fields and many of the fields

were sprayed with fungicides. Rust was found on most of the commonly grown cultivars. Numerous hot spots (foci) of rust infection were found throughout the area. In southeastern Arkansas, wheat plots of susceptible cultivars had 20–30 % stripe rust infection. There was a wide range in the amount of stripe rust on the cultivars in the breeding plots; some soft red winter wheat cultivars were highly resistant to stripe rust, whereas others were relatively susceptible. Stripe rust infections in Arkansas were scattered and light during the last week of April. In late May in west-central Missouri, 20 % wheat stripe rust severities were observed on flag leaves of soft red cultivars at the early berry stage. In mid-June fields of soft red winter wheat cultivars from northeastern Missouri to southern Indiana had 40–80 % stripe rust severities.

In both 2003 and 2002, stripe rust was severe in the soft wheat area growing areas of Arkansas and Missouri. Favorable weather conditions in 2003 and stripe rust inoculum from infection sites in Louisiana and Texas led to increased stripe rust in Arkansas and Missouri.

In mid-April, 20 % stripe rust severities were common in fields from northeastern Louisiana to central Georgia. However, the dry weather during the last 2 weeks of April slowed stripe rust development in many parts of the southern U.S. In late April in central Mississippi and central Alabama, wheat plots had stripe rust severities of 20 %. Infections were light in the commercial fields in this area. In mid-April, severe stripe rust was found in southern Georgia varietal plots at Plains with the most susceptible lines at 80–100 % severity. Entire plots were rusted indicating a uniform spore shower, not just isolated disease foci. Stripe rust (less than 5 % severity) also was found at Griffin, GA, 14 April on a few susceptible lines. By the end of the first week in May, stripe rust severities of 100 % were observed on susceptible cultivars in the south central Georgia wheat plots. This was the most severe wheat stripe rust ever seen in Georgia.

Midwest. In late May, stripe rust severities of 80 % were in a few fields in southern Illinois. In many of these wheat fields, stripe rust destroyed the flag leaves. In mid-June, from northwestern Ohio to north central Illinois, traces of stripe rust were observed in wheat fields. Stripe rust development in the northern soft red winter wheat growing area was greater than in 2002. Favorable weather conditions (cool temperatures and moisture) in 2003 and inoculum from many infection sites in the southern SRWW areas, allowed stripe rust to develop in the northern soft wheat area. The soft red winter wheat cultivars ranged from very resistant to fully susceptible to stripe rust.

East. In late May, wheat stripe rust foci were observed in plots at the Blacksburg Virginia experiment station. The incidence of stripe rust in the plots were trace to 5 %, whereas the severity in the major foci was 15–50 %. The Virginia cultivar Sisson that has the T1B-1R translocation had high stripe rust severity suggesting that stripe rust races with virulence to *Yr9* were common.

In early June, several major stripe rust foci and frequent secondary foci were found in the eastern shore nursery plots at Painter, Virginia. In mid-June, one small infection focus was found in plots in Warsaw, Virginia. Stripe rust was found throughout Virginia in 2003 but developed too late to cause significant damage to the wheat crop.

California. Stripe rust on wheat was first detected on 20 February in nurseries in Davis, CA, which was the earliest onset of stripe rust in a number of years. Infection foci were at 50 % severity. By late February, wheat stripe rust had increased on susceptible cultivars in nurseries and fields in the Sacramento Valley and was severe on early planted forage wheat (Dirkwin) in the northern San Joaquin Valley. Low levels of infection also were detected in wheat nurseries and commercial fields throughout the San Joaquin Valley on 4–5 March. Fields ranged from early joint to boot stage. In early April, wheat stripe rust infections had increased throughout much of the Central Valley of California and surrounding areas. Most of the current wheat cultivars in California, including many durum cultivars, are susceptible to stripe rust. A mild winter with moisture and early infection of very susceptible cultivars produced an abundant inoculum load. Susceptible cultivars, such as Dirkwin, Cavalier, Yecora Rojo, Eldon, Yolo, and Klasic had 100 % stripe rust severities. A larger proportion of wheat fields in California were sprayed with fungicides than in previous years. The fungicide Tilt was used early in the growing season but Quadris was applied after the emergence of the flag leaves.

In mid-April, in the Central Valley (Sacramento and San Joaquin valleys) of California, stripe rust was severe in plots of susceptible wheat cultivars. In the first week of May stripe rust was severe in fields in the Central Valley due to favorable conditions. By the fourth week in May, wheat stripe rust continued to increase on common and durum wheat in nurseries throughout the Central Valley of California. Stripe rust was more severe in California in 2003 than 2002, because the moist conditions and cool temperatures were very favorable for rust development throughout the growing season. Losses to stripe rust were significant this year in California (Table 4, p. 243).

Pacific Northwest. In late April, stripe rust was severe in susceptible winter wheat fields in southeastern Washington and northeastern Oregon. Infection foci with 60 % rust severities that were up to several hundred feet in diameter were found in wheat fields. The ground under the plants was covered with rust spores. Some fields in the area were sprayed with fungicides. By late April, stripe rust was also occurring on early-planted spring wheat cultivars in the Pendleton area of Oregon.

In 2003, in much of the Pacific Northwest, there were favorable conditions for over wintering of wheat stripe rust and the cool, moist conditions in late April and early May were favorable for rust development. In early May, severities of 90 % were observed on susceptible entries in the winter wheat nursery near Mt. Vernon in northeastern Washington. By mid-May, wheat stripe rust was severe in southeastern Washington winter wheat plots and fields. Many fields in eastern Washington were sprayed with fungicides. In irrigated spring wheat fields in southeastern Washington, rust severities of trace to 1 % were observed. Since abundant rust inoculum was in the region with favorable weather for rust development, stripe rust continued to spread and develop in eastern Washington and northern Idaho. By late May, 5–20 % wheat stripe rust severities were observed on susceptible winter wheat cultivars growing in fields and plots in the Palouse region of eastern Washington. In fields of SWWW, stripe rust infections were common, but most cultivars had resistant to moderately resistant reactions.

In mid-June, wheat stripe rust was developing rapidly in fields of susceptible spring wheat in eastern Washington. Some fields had incidence levels of 60 % stripe rust with severity levels up to 20 %. In mid-June, growers applied fungicides on susceptible spring wheat fields. In mid-June, 50 % severity levels were in irrigated plots of susceptible winter wheat cultivars in the dry land area of central Washington. Susceptible lines had 60 % severities in plots in a winter wheat nursery near Pullman, Washington, and fields in the area had only traces of rust. In July, dry conditions in Washington slowed stripe rust development.

NEBRASKA

**UNIVERSITY OF NEBRASKA–LINCOLN AND USDA–ARS, WHEAT, SORGHUM
& FORAGES UNIT
Lincoln, NE, 68583, USA.**

P.S. Baenziger, B. Beecher, D. Baltensperger, L. Nelson, I. Dweikat, M. Dickman, A. Mitra, T. Clemente, S. Sato, J. Watkins, J. Schimelfenig, and G. Hein (University of Nebraska); and R.A. Graybosch, L. Divis, R. French, and D. Stenger (USDA–ARS).

Production.

The 2003 Nebraska wheat crop was estimated at 79,900,000 bu, which represented a 47 bu/acre state average yield on 1,700,000 harvested acres. Acres planted to winter wheat in the autumn of 2002 were 1,800,000. The 2003 crop was 64 % larger than the 2002 crop, which was the smallest crop since 1944 and had the lowest yield since 1991. The 2003 crop had the highest yield since 1999 crop (86,400,000 bu from 1,800,000 harvested acres with a 48 bu/acre state average yield, which was a record).

Chromosome substitution lines.

P.S. Baenziger, K. Gill, K. Eskridge, Fufa Hundera Birru, I. Dweikat, and A. Mahmood.

This research was undertaken with the expectation as we learn more about the wheat genome; we would be able to develop better breeding strategies. The work was in collaboration with Kent Eskridge, Kulvinder Gill (now the Vogel Chair at Washington State University), and Ismail Dweikat. In 2003, the research of Fufa Hundera Birru, a Ph.D. student, and Abid Mahmood, a visiting scientist from Pakistan, provided new insight into how our cultivars were bred. Fufa studied the genetic diversity of 30 historical to modern wheat cultivars and found Cheyenne (CNN, believed to be the founding parent in our germ plasm) was closely related to Wichita. Both lines would be considered as being important ancestral parents of many Great Plains wheat cultivars. In previous studies, we determined that chromosome 3A of Wichita (WI) has very favorable genes for grain yield and agronomic performance. In preliminary studies, Dr. Mahmood studied the genetic diversity among chromosome 3A for 48 historic to modern wheat cultivars (including the 30 of Fufa's study) and found that no modern cultivar contained an intact CNN chromosome 3A, however, some modern cultivars contained a nearly intact WI chromosome 3A. Furthermore, when three genetic markers were used to study two previously identified regions containing favorable genes from WI, the cultivars could be grouped into those related to CNN (mainly western wheats where the WI genes had less value), to WI (mainly high yielding wheats where the genes should have value), and unrelated to CNN or WI, which we believe indicates new favorable alleles have been brought into our germ plasm for those genetic regions.

Wheat Transformation.

P.S. Baenziger, T. Clemente, S. Sato, J. Watkins, J. Schimelfenig, A. Mitra, and M. Dickman.

Wheat transformation continues to be a key strategic effort in the wheat improvement overall effort. In our current research, we are emphasizing trying to develop wheat lines with improved FHB resistance as part of the U.S. Wheat and Barely Scab Initiative. This study is a collaborative effort between T. Clemente and S. Sato of the Transformation Core facility (which does our wheat transformation), J. Watkins and J. Schimelfenig of the Department of Plant Pathology (who screen conventionally bred and transgenic wheat lines with FHB), and A. Mitra and M. Dickman, also of the Department of Plant Pathology, who are studying new concepts in disease resistance. So far, we have concentrated on transforming the following genes: a) inhibitors of apoptosis (programmed cell death) *ced9*, *IAP*, and *BCL X(L)*; b) lactoferrin and a related derived protein, lactoferricin; and c) related antifungal proteins that have been derived based on similar protein structures. Based on our greenhouse screening data, it appears that inhibitors of apoptosis, and lactoferrin and lactoferricin inhibit FHB, which indicates our concept is sound. We hope to retest the best lines in the field in 2004. The level of inhibition in our transgenic lines is generally less than that of Alsen (an elite FHB tolerant spring wheat with resistance derived from Sumai 3). We have begun crossing the best transgenes based on our greenhouse screening results into Alsen to see if we can improve upon the Sumai 3 resistance.

Fusarium head blight research.

P.S. Baenziger, T. Clemente, S. Sato, J. Watkins, J. Schimelfenig, A. Mitra, and M. Dickman.

In our research to lessen the potential devastating impact of FHB, we are complementing our transgenic wheat research with conventional breeding as part of the National Wheat and Barley Scab Initiative. Each year we are introgressing germplasm lines with FHB tolerance identified by the germ plasm screening efforts of the Initiative into our best lines. After repeated field testing, we have begun to identify Nebraska adapted lines with better FHB tolerance. These adapted lines will be used as parents in crosses with the germ plasm lines in hopes of increasing the level of tolerance above that of the germ plasm lines or the adapted lines. The adapted lines are:

ALLIANCE	=	ARKAN/COLT//CHISHOLM sib
ARAPAHOE	=	BRULE/3/PKR4*/AGENT//BELOT198/LCR
CULVER	=	NE82419 X ARAPAHOE
GOODSTREAK	=	SD3055/KS88H164//NE89646 (=COLT*2/PATRIZANKA)
N97V121	=	N87V106/OK88767

NE00403	=	PRONGHORN/ARLIN//ABILENE
NE00544	=	SD89180/KARL 92
NE99579	=	TOMAHAWK/PRONGHORN//NE89657
NIOBRARA	=	TAM105*4/AMIGO (TX80GH2679)//BRULE Fsel
WESLEY	=	KS831936-3//COLT/CODY

Arapahoe is a parent in many of our modern cultivars and Wesley and Culver are cultivars that are widely grown in the regions that are most likely to have FHB epidemics. Hence, producers can reduce the risk of FHB while growing excellent lines.

Winter triticale.

P.S. Baenziger.

In 2003, NE95T426 (WB-UW24/TxTcl #50//Fain Tcl/Ctk 78//NE69150/6TA876 / Unknown (probably 6A365/NE69150) was recommended for release and the first commercial foundation seed sales were made. WB-UW24 is a line of unknown pedigree that was sent to the program in the late 1980s as part of an international nursery. NE95T426 will be released at NE426GT and co-released with Iowa State University. The GT designation is in recognition that it can be used either as a autumn and early spring forage triticale (determined by Carlyle Thompson of Kansas State University, Hays, KS whose help and interest in fostering triticale production is invaluable) or as a grain triticale. NE426GT is expected to be mainly used in Nebraska in forage blends with our forage triticales (which are haying or spring forage types), so that the blend will have good autumn and spring forage potential and will have less costly to produce. Excellent collaborations were established with a team of triticale researchers at Iowa State University (the breeder is Jean-Luc Jannink) who are interested in grain triticale to diversify their cropping systems. In Iowa, NE426GT is expected to mainly be used as a grain triticale for animal feed. Although the future is always uncertain, triticale is being given a careful look to determine if it can aid producers. With the retirement of Carlyle Thompson, triticale has lost a great friend and champion.

Hard white wheat development.

R.A. Graybosch, P.S. Baenziger, B. Beecher, D. Baltensperger, and L. Nelson.

The HWWs Antelope (NW97S278) and Arrowsmith (NW97S182) were approved for release, and Foundation seed production is underway. The following HWWs were advanced to the Nebraska Statewide Small Grains Variety trial for additional testing: NW99L7068, NW97S412-1, NW97S139-1, NW98S097, and NW97S218-lt.

Wheat germ plasm releases.

R.A. Graybosch and P.S. Baenziger.

PI 617069 (96MD7413-58), PI 617070 (96MD7413-36), and PI 617071 (96MD7110-71) partial waxy (reduced amylose) hard winter wheat germ plasm lines were released by the Agricultural Research Service, United States Department of Agriculture, and the Nebraska Agricultural Experiment Station. These partial waxy wheats carry nonfunctional (null) alleles (*Wx-A1b*, and *Wx-B1b*) at two of the three hexaploid wheat *Wx* loci. These loci encode isoforms of the enzyme granule-bound starch synthase (GBSS, EC 2.4.1.21), also known as the waxy protein. Wheats with nonfunctional alleles at two loci are known as double-nulls. Double-null, partial waxy wheats produce endosperm starch with reduced amylose content, relative to that of single-null or wild-type wheats.

Breeding of WSMV-resistant winter wheat.

L.A. Divis, R. Graybosch, P.S. Baenziger, and G. Hein.

Wheat streak mosaic virus is one of the most important diseases affecting winter wheat in the western Great Plains of North America. No known resistance to WSMV exists in the primary gene pool of wheat. However, a resistance gene known as *Wsm1*, has been transferred to wheat from perennial relatives. Nebraska-adapted wheat lines carrying the gene *Wsm1*, conditioning resistance to WSMV, were used in this study. Sister-lines from six genetic populations were analyzed to compare agronomic and quality characteristics of resistant and susceptible lines in the absence of the virus, and under a naturally occurring viral infection. Seed composites from the same randomly selected lines across uninfected locations were used for quality analyses. Over all populations, there was no significant difference in yield, but resistant lines had significantly higher test weight in the uninfected locations. Within each population, significant differences in yield were observed only in population 1, whereas significant differences in test weight occurred in populations 1, 2, 5, and 6. At the infected location, resistant lines were significantly higher in yield in five of six populations. Over all populations, susceptible lines were significantly higher in loaf volume and percent water absorption, while flour protein content was significantly higher in two populations. The *Wsm1* gene is beneficial when the virus is present, and there seems to be no yield detriment in the absence of the virus.

Personnel.

Mr. Chris Hoagland left his technologist position to join the USDA in Pullman, WA. Mr. Jerry Bohlmann joined the project as a technologist. Mr. Lekgari A. Lekgari joined the project as a graduate student. Dr. Abid Mahmood completed his year as a visiting scientist with Drs. Baenziger and Dweikat to learn molecular biology and returned to Pakistan. Dr. Bakytzhan Anapiyayev and his student, Mr. Daulet Satybaldiyev, from Kazakhstan visited the laboratory of Dr. Dweikat to learn molecular marker skills.

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NORTH DAKOTA

USDA–ARS CEREAL CROPS RESEARCH UNIT Northern Crop Science Laboratory, Fargo, ND, USA.

Justin D. Faris, Timothy Friesen, Steven Xu, Shaukat Ali, Erik Doehler, Elias M. Elias, Karri M. Haen, G.A. Hareland, Jinguo Hu, Leonard Joppa, Khalil Kahn, Daryl Klindworth, Zhaohui Liu, Huangjun Lu, Steven W. Meinhardt, James Miller, Gloria Nygard, Jack B. Rasmussen, and Kristin Simons.

The construction of a BAC contig for chromosome walking at the Tsn1 locus in wheat.

Huangjun Lu, Karri M. Haen, John P. Fellers, Timothy L. Friesen, Steven W. Meinhardt, and Justin D. Faris.

Tsn1 conditions sensitivity to a host-selective proteinaceous toxin (Ptr ToxA) produced by the pathogenic fungus *Pyrenophora tritici-repentis* and plays an important role in pathogen-host recognition. A large F₂ population consisting of 5,450 gametes was produced to develop a high-resolution map for positional cloning of the gene. High-resolution mapping delineated the *Tsn1* gene to a 0.55 cM interval flanked by AFLP-derived markers *Xfcg17* and *Xfcg9* at 0.15 and 0.41 cM from the gene, respectively. More tightly linked markers were developed using chromosome walking in

conjunction with complete sequencing of BACs identified in the Langdon durum BAC library. Although the *Tsn1* gene lies within a recombination hot spot along the chromosome, our results indicate that recombination frequencies vary significantly within the BAC contig. From the regions that have been sequenced, we identified more than 10 genes, most of which are genes that encode cell wall-associated receptors or kinases. The product of the *Tsn1* gene also may be a cell wall-associated protein that interacts with the toxin to manifest necrosis because plants having *tsn1* or the null allele (deletion lines) are insensitive to Ptr ToxA. The cloning and characterization of *Tsn1* will be helpful in better understanding the host-pathogen interaction.

Molecular cloning of the Q locus in wheat.

Kristin Simons, John P. Fellers, Harold Trick, Bikram S. Gill, and Justin D. Faris.

The *Q* locus played a major role in the domestication of polyploid wheat because it confers the square-headed phenotype and the free-threshing character, and it pleiotropically influences many other agronomically important traits. A physical contig spanning the *Q* locus on chromosome 5A was constructed using a *T. monococcum* BAC library. The 100-kb segment cosegregating with *Q* contained an *APETELA2* (*AP2*)-like gene. This gene is a likely candidate for *Q*, because *AP2* plays a major role in controlling floral homeotic gene expression in *Arabidopsis*. The *AP2*-like gene was sequenced from the free-threshing *T. aestivum* cultivar Chinese Spring, the free-threshing *T. turgidum* cultivar Langdon, and several nonfree-threshing wild relatives. Sequence comparisons revealed slight differences between free-threshing and nonfree-threshing species. EMS-treated *T. aestivum* lines were screened for mutations in the *Q* locus. Of six mutant lines, three were the result of large deletions encompassing the *Q* locus. The *AP2*-like gene in the remaining three lines had base substitutions that resulted in coding of a different amino acid or the alteration of a predicted exon/intron splice site. Transgenic individuals were created using a 5 kb subclone of a *T. turgidum* BAC containing the *Q* locus. These transgenic individuals mimicked the increased or decreased dosage effect of *Q*, suggesting the occurrence of silencing and over-expression, respectively.

Molecular mapping of resistance to Pyrenophora tritici-repentis race 5 and sensitivity to PtrToxB in wheat.

Justin D. Faris and Timothy L. Friesen.

Tan spot is an economically important foliar disease in the major wheat growing areas of the world. Multiple races of the pathogen have been characterized based on their ability to cause necrosis and/or chlorosis on differential wheat lines. Isolates of race 5 cause chlorosis only, and they produce a host-selective toxin designated Ptr ToxB that induces chlorosis when infiltrated into sensitive genotypes. We used the ITMI mapping population to identify genomic regions harboring QTL for resistance to fungal inoculations of PTR race 5 and to determine the chromosomal location of the gene conditioning sensitivity to Ptr ToxB. The toxin-sensitivity gene mapped to the distal tip of the short arm of chromosome 2B. This gene was responsible for the effects of a major QTL associated with resistance to the race 5 fungus and accounted for 69 percent of the phenotypic variation. Additional minor QTL were identified on the short arm of 2A, the long arm of 4A, and elsewhere on chromosome 2B. A multiple regression model consisting of the major QTL on 2BS identified by the toxin insensitivity gene, a marker underlying a minor QTL on 2B, a marker on 4AL, and an epistatic interaction accounted for 76 percent of the total phenotypic variation for resistance to PTR race 5. The results of this research indicate that Ptr ToxB is a major virulence factor, and the markers underlying significant QTL should be useful for introgression of resistance into adapted germ plasm.

Genetic and physical mapping of a gene conditioning sensitivity in wheat to a partially purified host-selective toxin produced by Stagonospora nodorum.

Zhaohui Liu, Justin D. Faris, Steven Meinhardt, Shaukat Ali, Jack B. Rasmussen, and Timothy L. Friesen.

Stagonospora nodorum is the causal agent of wheat leaf and glume blotch, an economically important disease in many wheat-growing areas throughout the world. Using filtration, ion-exchange and gel-filtration chromatography, we

partially purified a toxin from culture filtrates of isolate Sn2000. This toxin, designated as SnTox1, showed selective action on several different wheat genotypes indicating that it is a host-selective toxin (HST). The ITMI mapping population was evaluated for toxin reaction and used to map the host gene conditioning sensitivity. This gene, designated as *Snn1*, was genetically mapped to the distal end of chromosome 1BS. The wheat cultivar Chinese Spring and all CS nullisomic-tetrasomic lines were sensitive to the toxin, with the exception of N1BT1D. Insensitivity also was observed when the 1B chromosome of CS was substituted by the 1B chromosome of an insensitive accession of *Triticum dicoccoides*. These results indicate that the toxin sensitivity gene resides on chromosome 1B, and suggest that sensitivity is dominant. A series of 1BS deletion lines were used to physically localize the sensitivity gene. Physical mapping indicated that *Snn1* lies within a major gene-rich region on 1BS.

QTL analysis and mapping of resistance to Stagonospora nodorum leaf blotch in wheat.

Zhaohui Liu, Tim L. Friesen, Steven Meinhardt, Shaikat Ali, Jack B. Rasmussen, and Justin D. Faris.

Stagonospora nodorum leaf blotch (SNB) is an economically important foliar disease in the major wheat-growing areas of the world. Utilization of host resistance is considered to be the most important and preferred method to control disease. In related work, we identified a host-selective toxin (SnTox1) produced by the isolate Sn2000 and mapped the gene (*Snn1*) conditioning sensitivity to chromosome 1BS. Here, we screened the ITMI mapping population and cytogenetic stocks, including nullisomic-tetrasomic lines and CS–*T. dicoccoides* (CS–DIC) substitution lines, with isolate Sn2000 to identify QTL associated with resistance to SNB. QTL analysis revealed that *Snn1* underlies a major QTL and explained 58.3, 47.7, and 27 percent of the phenotypic variation for 5, 7, and 10-day readings, respectively. This 1BS QTL, a minor QTL on chromosome 4BL, and an interaction between *Snn1* and a marker on chromosome 2B, explained as much as 66 percent of the total phenotypic variation. An additional QTL on chromosome 7BL was identified for the 10-day readings. Toxin sensitivity was highly correlated with chlorotic flecking on the leaves, which occurred in the early stages of disease development. N1BT1D and CS–DIC 1B were absent of chlorotic flecking and less susceptible to the fungus. These results in combination with the decreased effects of the 1BS QTL from 5 to 7 to 10 days indicate that the toxin is a major virulence factor, and is most effective in the early stages of the interaction.

Evaluation of synthetic hexaploid wheats for seedling resistance to tan spot and Stagonospora nodorum blotch.

Steven S. Xu and Timothy L. Friesen.

Production of synthetic hexaploid wheat (SHW or synthetic) lines ($2n = 6x = 42$, AABBDD) is a practical way to generate a useful germ plasm source for the transfer of desirable traits from *Ae. tauschii* and tetraploid wheat to bread wheat. The Wide Hybridization Program at CIMMYT recently selected and characterized two sets of elite SHW lines (Elite 1 and Elite 2). Thus far, some important traits such as agronomic performance, quality traits, and resistance to various diseases have been evaluated. However, their resistance to tan spot and SNB has not been evaluated. Tan spot and SNB are important foliar diseases of bread wheat and durum wheat. These two diseases have ability to cause serious yield losses. Because the majority of current bread and durum wheat cultivars are susceptible, there is a need to find new sources of high level resistance to tan spot and SNB and transfer the resistance to local cultivars. In this study, 120 elite CIMMYT SHW lines and their durum wheat parents were inoculated with *P. tritici-repentis* race 1 and a standard field isolate (Sn2000) of *S. nodorum*, respectively, in two separate, three-replication experiments. The seedling reactions to *P. tritici-repentis* and *S. nodorum* were evaluated 7 and 10 d postinoculation, respectively. The plant leaves also were infiltrated with the host selective toxin Ptr ToxA at the two-leaf stage and sensitivity was evaluated 3–4 d post infiltration. As expected, most SHW lines were the same as their durum parents in their sensitivity to Ptr ToxA, because the sensitivity locus *Tsn1* is located on chromosome 5B. However, a few of the synthetics were different from their durum parents, suggesting that heterozygosity and heterogeneity might exist in some of the SHW lines and durum parents. The toxin sensitivity significantly increased susceptibility of the synthetics to tan spot but had no significant effects on durum parents. The data showed that 56 (46.7 %) and 36 (30.0 %) SHW lines were resistant to tan spot and SNB, respectively, whereas resistance was almost absent in the durum parents. These results suggest that the elite CIMMYT synthetics are an excellent source of new resistance to tan spot and SNB and should be useful in developing new resistant cultivars and adapted germplasm in bread wheat.

Chromosomal locations of novel glutenin subunits and gliadins in wild emmer wheat.

Steven S. Xu, Khalil Khan, Daryl L. Klindworth, Justin D. Faris, Gloria Nygard.

Triticum turgidum subsp. *dicoccoides* (DIC), known as wild emmer, is the tetraploid progenitor of durum and bread wheat. Wild emmer has many useful traits such as pest resistance, high protein content, and unique protein compositions. The glutenin and gliadin proteins of wild emmer wheat have potential for improvement of durum wheat quality. The objective of this study was to determine the chromosomes controlling the high molecular weight (HMW) glutenin subunits and gliadin proteins present in three *T. turgidum* subsp. *dicoccoides* accessions (Israel-A, PI-481521, and PI-478742), which were used as chromosome donors in Langdon durum-*T. turgidum* subsp. *dicoccoides* (LDN-DIC) chromosome substitution lines. The three *T. turgidum* subsp. *dicoccoides* accessions, their respective LDN-DIC substitution lines, and a number of controls with known HMW-glutenin subunits were analyzed by SDS-PAGE, Urea/SDS-PAGE, and A-PAGE. The results revealed that all three *T. turgidum* subsp. *dicoccoides* accessions possess *Glu-1A* alleles that are the same as or similar to those reported previously. However, each *T. turgidum* subsp. *dicoccoides* accession had a unique *Glu-B1* allele. The new *Glu-B1* alleles were designated as *Glu-B1be* in Israel-A, *Glu-B1bf* in PI-481521, and *Glu-B1bg* in PI-478742. Results from A-PAGE indicated that there were eight, twelve, and nine unique gliadin proteins bands, which were assigned to specific chromosomes, in PI-481521, PI-478742, and Israel-A, respectively. The identified glutenin and gliadin proteins in the LDN-DIC substitution lines provide the basis for evaluating their effects on end-use quality, and they are also useful biochemical markers for identifying specific *T. turgidum* subsp. *dicoccoides* chromosomes or chromosome segments.

Agronomic and quality characteristics of TIAS-1AL-1DL translocation lines of durum wheat carrying Glu-D1d.

Daryl L. Klindworth, Gary A. Hareland, Elias M. Elias, and Steven S. Xu.

Markets for durum wheat could be expanded if cultivars with dual-purpose end-use could be developed. The *Glu-D1d* allele encoding glutenin subunits 5+10 imparts good baking quality to hexaploid wheat. The objective of this study was to test the agronomic and baking quality of TIAS-1AL-1DL translocation lines of durum wheat with *Glu-D1d*. Translocation lines were classified according to the presence of either low-molecular weight I (LMWI; weak gluten) or LMWII (strong gluten) banding patterns conditioned by the *Glu-B3* locus. Advanced generation translocation lines in a Renville background were grown in yield trials conducted at two locations in North Dakota from 1998 through 2002. Translocation lines were milled and mixing and baking characteristics determined. Only two translocation lines did not differ statistically from Renville for yield and were similar to Renville for lodging score, heading date, and plant height. The translocation lines had reduced thousand kernel weight and a high 'G x E' interaction for farinogram characteristics. Compared to Renville, mean loaf volumes were not improved. Translocation lines having LMWI had better mixing stability and loaf volume than lines having LMWII. Although the results suggest agronomic traits can be sufficiently improved, commercial production of the translocation lines may not be feasible without more consistent mixing traits and improved baking characteristics.

High-throughput marker identification and mapping in wheat using TRAPs (Target Region Amplification Polymorphism).

Justin D. Faris, Steven S. Xu, Zhaohui Liu, and Jinguo Hu.

High-throughput marker technologies are necessary for the rapid mapping of plant genomes to identify genomic regions harboring genes governing desirable traits and for marker-assisted selection. The recently developed TRAP technique employs an 18mer random primer in combination with a fixed 18mer primer designed based on known EST sequences to amplify genomic fragments. The random primers are 3' end-labeled with IR dye 700 or IR dye 800 for autodetection on a Li-Cor Global DNA Sequencer. We applied the TRAP technique to two sets of tetraploid Langdon durum-*T. turgidum* subsp. *dicoccoides* (LDN-DIC) disomic chromosome substitution lines to determine the number and chromosomal locations of polymorphic TRAP markers. The LDN-DIC (PI481521) disomic substitution set has been characterized with 37 PCR reactions resulting in the identification of 642 TRAP markers. The markers were distributed among all 14 chromosomes, and the number per chromosome ranged from 19 (3B) to 72 (7A). The second disomic substitution set

[LDN-DIC (PI4787420)] has been partially characterized with 91 polymorphic markers identified from five PCR reactions. On average, 17 polymorphic markers were observed per PCR reaction in the LDN-DIC lines. In addition, we assessed the number of polymorphic markers and genetic map locations of TRAPs in a hexaploid wheat recombinant inbred population derived from 'BR34/Grandin'. In this population, we observed an average of 20 polymorphic markers per PCR reaction. The TRAP markers are useful for genome characterization, tagging desirable genes, and high-throughput mapping of wheat populations.

Genetic stocks and germ plasm in tetraploid and hexaploid wheat available for distribution.

Steven S. Xu, Justin D. Faris, Daryl L. Klindworth.

The mission of our wheat germ plasm enhancement program primarily includes the development and characterization of new genetic stocks and germ plasm in durum and hard red spring wheat. Leonard R. Joppa (ARS retired) and the late Norman D. Williams developed a number of valuable genetic stocks and germ plasms using classical cytogenetic approaches. Many of them have not been characterized and released to the public. We have engaged in efforts in characterizing these materials using molecular cytogenetics and DNA marker technologies. Some of these lines also have been recently evaluated for resistance to various diseases, Hessian fly, and seed-storage-protein compositions. Here, we summarize the genetic stocks and germ plasm available for distribution. We are able to provide a small seed sample (20–30 seeds/line) upon request.

Langdon durum–*T. turgidum* subsp. *dicoccoides* disomic substitution lines. Three sets of Langdon durum–*T. turgidum* subsp. *dicoccoides* (LDN-DIC) disomic substitution lines were developed by L.R. Joppa using *T. turgidum* subsp. *dicoccoides* accessions Israel-A, PI481521, and PI478742 as the chromosome donor in Langdon background. The set based on PI481521 has all 14 chromosome substitutions available, but

Table 1. Langdon durum–*Aegilops tauschii* synthetic hexaploid wheats.

Line #	Pedigree	Source of <i>Ae. tauschii</i>
1	Langdon/ <i>Ae. tauschii</i> CI 00001	NSGC, Aberdeen, Idaho
2	Langdon/ <i>Ae. tauschii</i> CI 00005	NSGC, Aberdeen, Idaho
3	Langdon/ <i>Ae. tauschii</i> CI 00009	NSGC, Aberdeen, Idaho
4	Langdon/ <i>Ae. tauschii</i> CI 00011	NSGC, Aberdeen, Idaho
5	Langdon/ <i>Ae. tauschii</i> CI 00014	NSGC, Aberdeen, Idaho
7	Langdon/ <i>Ae. tauschii</i> CI 00022	NSGC, Aberdeen, Idaho
8	Langdon/ <i>Ae. tauschii</i> CI 00025	NSGC, Aberdeen, Idaho
9	Langdon/ <i>Ae. tauschii</i> CI 00026	NSGC, Aberdeen, Idaho
10	Langdon/ <i>Ae. tauschii</i> H80-101-4	Haifa, Israel
11	Langdon/ <i>Ae. tauschii</i> H80-114-1	Haifa, Israel
12	Langdon/ <i>Ae. tauschii</i> H80-115-3	Haifa, Israel
14	Langdon/ <i>Ae. tauschii</i> PI 220641	NSGC, Aberdeen, Idaho
16	Langdon/ <i>Ae. tauschii</i> RL 5003	Winnipeg, Manitoba, Canada
17	Langdon/ <i>Ae. tauschii</i> RL 5214	Winnipeg, Manitoba, Canada
19	Langdon/ <i>Ae. tauschii</i> RL 5259	Winnipeg, Manitoba, Canada
20	Langdon/ <i>Ae. tauschii</i> RL 5261	Winnipeg, Manitoba, Canada
21	Langdon/ <i>Ae. tauschii</i> RL 5263	Winnipeg, Manitoba, Canada
22	Langdon/ <i>Ae. tauschii</i> RL 5266-1	Winnipeg, Manitoba, Canada
23	Langdon/ <i>Ae. tauschii</i> RL 5271	Winnipeg, Manitoba, Canada
24	Langdon/ <i>Ae. tauschii</i> RL 5272	Winnipeg, Manitoba, Canada
25	Langdon/ <i>Ae. tauschii</i> RL 5286	Winnipeg, Manitoba, Canada
26	Langdon/ <i>Ae. tauschii</i> RL 5392	Winnipeg, Manitoba, Canada
27	Langdon/ <i>Ae. tauschii</i> RL 5393	Winnipeg, Manitoba, Canada
28	Langdon/ <i>Ae. tauschii</i> RL 5492	Winnipeg, Manitoba, Canada
29	Langdon/ <i>Ae. tauschii</i> RL 5498	Winnipeg, Manitoba, Canada
30	Langdon/ <i>Ae. tauschii</i> RL 5527	Winnipeg, Manitoba, Canada
32	Langdon/ <i>Ae. tauschii</i> RL 5532	Winnipeg, Manitoba, Canada
34	Langdon/ <i>Ae. tauschii</i> RL 5544	Winnipeg, Manitoba, Canada
35	Langdon/ <i>Ae. tauschii</i> RL 5552	Winnipeg, Manitoba, Canada
36	Langdon/ <i>Ae. tauschii</i> RL 5555	Winnipeg, Manitoba, Canada
38	Langdon/ <i>Ae. tauschii</i> RL 5560	Winnipeg, Manitoba, Canada
39	Langdon/ <i>Ae. tauschii</i> RL 5561	Winnipeg, Manitoba, Canada
40	Langdon/ <i>Ae. tauschii</i> RL 5562	Winnipeg, Manitoba, Canada
41	Langdon/ <i>Ae. tauschii</i> RL 5570	Winnipeg, Manitoba, Canada
44	Langdon/ <i>Ae. tauschii</i> PI 476874	NSGC, Aberdeen, Idaho
52	Langdon/ <i>Ae. tauschii</i> CI 00017	NSGC, Aberdeen, Idaho
53	Langdon/ <i>Ae. tauschii</i> PI 268210	NSGC, Aberdeen, Idaho
55	Langdon/ <i>Ae. tauschii</i> RL 5257	Winnipeg, Manitoba, Canada
56	Langdon/ <i>Ae. tauschii</i> RL 5258	Winnipeg, Manitoba, Canada
57	Langdon/ <i>Ae. tauschii</i> RL 5270	Winnipeg, Manitoba, Canada

the substitution for chromosome 2B for the set based on Israel-A and three substitutions (2A, 3A, and 3B) in the set based on PI478742 are not available.

Langdon durum-*Ae. tauschii* SH wheat. Dr. Leonard R. Joppa developed a number of spontaneous synthetic hexaploid wheat from partially fertile hybrids between LDN and different *Ae. tauschii* accessions in the 1980s. We recently developed a new synthetic line from a cross between LDN and *Ae. tauschii* PI476874, which has a tough rachis. Some *Ae. tauschii* accessions were received from National Small Grains Collection (NSGC), Aberdeen, ID, others were provided respectively by E.R. Kerber (Agriculture and Agri-Food Canada, Winnipeg, Manitoba, Canada) and E. Nevo (University of Haifa, Haifa, Israel). Except for the synthetic line from cross 'LDN/PI 268210' was named as Largo and released as greenbug-resistant germ plasm, other lines have not been characterized previously. These synthetics have recently been evaluated for resistance to tan spot, SNB, leaf and stem rust, and Hessian fly. We currently are evaluating their resistance to FHB and seed-storage protein compositions. The synthetics that are available for seed distribution are listed in Table 1 (p. 256).

Durum wheat T1AS·1AL·1DL translocation lines carrying *Glu-D1d*. Four translocation lines with the pedigree 'LDN 1D (1A)/LEN//LDN/3/2*Renville' and with glutenin subunits 1Dx5 and 1Dy10 from the *Glu-D1d* allele are available. These lines were produced in an effort to develop dual-purpose (good baking and pasta quality) durum wheat. The lines are identified as L092, L252, S99B33, and S99B34. Three of the lines carry the LMWII-banding pattern derived from Renville and conditioned by the *Glu-B3* gene. The fourth line, L252, carries the LMWI-banding pattern derived from LDN. Quality tests have indicated L252 has better mixing traits and slightly better loaf volume than the translocation lines with LMWII. In trials conducted in North Dakota from 2000–02, S99B33 and S99B34 were the highest yielding of the translocation lines and similar in yield to Renville. These lines should be useful to breeders attempting to produce dual-purpose durum or for cereal chemists studying effects of *Glu-D1d* in a durum background.

Induced mutants in hexaploid and tetraploid wheat and miscellaneous stocks. N.D. Williams induced many mutants in hexaploid and tetraploid wheat, primarily through application of EMS to seeds. Male-sterile mutants in hexaploid wheat include the FS2, FS3, FS6, FS20, and FS24 mutants that have been reported in the literature. Additional recessive male sterile mutants that have not been reported in the literature are also available, and all are known to be allelic to either *ms1* or *ms5*. Chlorina mutants are available in both hexaploid and tetraploid wheat that have been reported in the literature. Additional abnormal chlorophyll mutants, such as virescent and albino, genetics have not been studied. Lines derived from conventional breeding techniques include a durum line carrying the blue aleurone trait and lines carrying genes conditioning the branched spike trait in durum wheat.

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OKLAHOMA**OKLAHOMA STATE UNIVERSITY****Department of Plant and Soil Sciences, 368 Ag Hall, Stillwater, OK 74078-6028, USA.**

B.F. Carver, A.K. Klatt, and A.C. Guenzi.

Cultivar development and breeding research.

Brett F. Carver.

We continue to follow a modified bulk-pedigree selection method, whereby early generation (F_2 – F_4) populations are selected and advanced as bulk populations, lines are derived from F_4 populations as head rows, and subsequent generations are advanced primarily through line-selfing. Critical to this program is what we have coined the **GRAZENGRAIN** breeding system, instituted in 1997, which now generates all of the breeder lines for statewide replicated yield trials. This breeding system interweaves two components throughout the 10-year variety development cycle: 1) multi-environment selection procedures common to any wheat-breeding program and 2) management system-targeted selection (dual-purpose and grain-only systems). The second component expands the scope of environments to which our materials are subjected and the portfolio of traits by which our materials are selected. The result is a collection of breeding lines with potentially broader adaptation than selection in the absence of a management system component. This breadth of adaptation is needed by wheat producers in the southern Great Plains if they continue to use cultivars nondiscriminately in grain-only and early-planted, forage-based, production systems.

Feeding the OSU breeding pipeline is a crossing program that features a 1:2 ratio of single (adapted/ adapted) and three-way crosses (typically adapted/non-adapted//adapted). Additional crosses enter the pipeline midstream from Bob Hunger, Department of Entomology and Plant Pathology, and Art Klatt, Department of Plant and Soil Sciences, whose report follows this one. Depending on the generation of breeding and the environment, selection decisions revolve on a ring of six trait complexes: 1) adaptation, 2) disease resistance, 3) insect resistance, 4) stress tolerance, 5) grain quality, and 6) functionality. Specific target traits are identified for each complex on our website, www.wit.okstate.edu. Traits that form the bulls-eye of all agronomic targets are resistance to leaf rust, stripe rust, and WSBMV, tolerance to low-pH soils, and reduced yield loss after autumn and winter grazing, whereas those constituting the bulls-eye of all quality targets include test weight, kernel size, protein content, and dough strength.

The Oklahoma Agricultural Experiment Station and USDA–ARS will jointly announce in May 2004 the release of **Endurance** and **Deliver** HRWW. Endurance originated in the wheat breeding program of Pioneer Hi-Bred International, Inc., and was tested under the experimental name, OK94P549-11 (pedigree: HBY756A/Siouxland//2180). Of the approximately 12 cultivars expected to occupy the most wheat acreage in Oklahoma in the next 5 years, eight are considered so early in first-hollow-stem (FHS) development to present adverse risk in grain production under the most predominant management system used in the southern Great Plains. Yield protection in a dual-purpose system may require various system-specific adaptations, but one that appears highly consequential is the capacity to remain vegetative throughout the winter grazing season. Endurance maintains a vegetative growth habit longer than most cultivars without delay in heading date. With this cultivar, the winter grazing season may be extended by as much as 2 weeks beyond early-FHS cultivars, with only minimal yield loss in the dual-purpose system (3%) compared to a grain-only system. Other favorable attributes are adult-plant resistance to wheat leaf rust races currently present in Oklahoma, moderate adult-plant resistance to wheat stem rust, and an intermediate to resistant reaction to wheat stripe rust. It also renders protection against highly acidic soils present in Oklahoma. Kernel size attributes, flour extraction, and flour ash content place Endurance in a desirable category for milling quality.

Deliver was tested under the experimental name, OK98690, and originates from the cross ‘OK91724 (=Yantar/2*Chisholm)/Karl’. Because Deliver, an awnletted wheat, will be recommended for a dual-purpose system, a grain-only system, or a hay-production system, this tri-purpose wheat will provide producers flex-management options they currently lack with awned grain-type cultivars or awnletted forage-type cultivars. Flexibility derives from the ability to

make in-season decisions on using a standing crop for grain production or for hay or late-season grazing. Deliver possesses moderate to substantial improvement in grain yield potential over currently grown cultivars and recently released cultivars yet to gain significant acreage, outstanding test weight patterns combined with unusually large kernel size, consistently high forage availability throughout the winter grazing season combined with a relatively late FHS date, broad-spectrum adult-plant resistance to the major foliar diseases in Oklahoma (leaf rust, stripe rust, WSBMV, and Septoria), and above-average milling and baking quality. Weaknesses include moderate susceptibility to lodging and to acid soils. Deliver consistently ranked as one of our best breeding lines from 2000 to 2003 for kernel weight (1,000-kernel weight = 31.5 g) and kernel size (kernel diameter = 2.36 mm and large kernel fraction = 76 %). That these attributes were recorded on an awnleted wheat in Oklahoma makes them even more unusual.

Variability enhancement/germ plasm development.

Arthur K. Klatt.

A major breeding effort is ongoing at OSU to incorporate new genetic diversity into the winter wheat improvement program. This variability enhancement program makes extensive use of spring wheat materials from CIMMYT and advanced lines from winter wheat-breeding programs in the region as the primary sources of genetic diversity. All introductions are screened for multiple disease resistance and agronomic type in Oklahoma and at a special coöperative disease nursery in south Texas, and the best materials are incorporated into the crossing program. The fifth cycle of crossing is currently in progress.

Winter wheat cultivars with stable, long-term leaf rust resistance have not been identified for the southern and central Great Plains. A new variety typically maintains leaf rust resistance for a short period of time (2–4 years). In recent years, stripe or yellow rust has caused significant production losses, and advanced lines in many programs lack good resistance. As a result, the breeding programs in the region must devote extensive resources to incorporate new genes for leaf rust resistance and to the development of adapted materials with good yellow rust resistance. A primary objective of the variability enhancement/germplasm development program at OSU is to transfer durable leaf rust and durable yellow rust resistance from CIMMYT spring wheat germ plasm into adapted winter wheat cultivars. Durable or slow rusting resistance is characterized by low levels of infection and is generally based on one or more major genes plus several minor genes. Additionally, an extensive crossing program to synthetics and synthetic derivatives developed by CIMMYT is underway. This effort has multiple objectives, including potentially new genes for leaf and yellow rust resistance, improved kernel size, enhanced stay green characteristics, and improved biomass and yield potential. For information regarding this program, contact Dr. Art Klatt, Dept. of Plant and Soil Sciences, 274 Ag Hall, Stillwater, OK 74078 or via EMAIL at aklatt@mail.pss.okstate.edu.

Differential gene expression in wheat roots in response to infection by soilborne pathogens.

Arron C. Guenzi.

Coöperating in this project are Tim D. Samuels, J. Larry Green, G. Charmaine Naidoo, Larry Singleton, and Trish Ayoubi¹ from Oklahoma State University, and John P. Fellers with USDA–ARS, Manhattan, KS, and Robert A. Gonzales with Samuel Roberts Noble Foundation, Ardmore, OK.

A systematic characterization is ongoing to define transcription profiles between the interactions of wheat roots of the cultivar Jagger and 1) *G. graminis*, 2) *Rh. solani*, and 3) *P. arrhenomanes*. These three species represent a complex of soilborne pathogens (i.e., the root-rots) that are endemic to all wheat producing regions in the Great Plains and much of the world. The severity of infection, and subsequent yield loss, can vary greatly between years and even within a given field. These diseases represent a largely under-researched class of diseases because of the difficulty in studying roots. As a result of this out-of-sight/out-of-mind phenomenon, the chronic loss due to these soilborne pathogens is probably grossly underestimated. Loss due to root-rots is also increased with the early planting associated with production of dual-purpose wheat. The most dramatic illustration of the chronic stress due to soilborne fungi is the dramatic increase in wheat yields; nearly two fold, associated with sterilizing soil in replicated field plots with methyl bromide.

A cDNA microarray representing genes differentially expressed during early stages of infection was created and used to characterize host transcription profiles during root surface colonization, epidermis penetration, and cortex colonization. The array consists of 4,200 elements that were replicated three times. One hundred and fifty genes were differentially expressed during the wheat *G. graminis* interaction. One hundred and five genes were differentially expressed during the infection by *P. arrhenomanes* into wheat roots. Surprisingly, there was little overlap between the gene expression profiles for these two pathogens with the same host genotype. These results provide targets for future functional analyses to dissect the biology of these diseases.

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SOUTH DAKOTA

SOUTH DAKOTA STATE UNIVERSITY AND THE USDA-ARS NORTHERN GRAIN INSECT RESEARCH LABORATORY (NGIRL). Plant Science Department, Brookings, SD 57007 U.S.A.

A.M.H. Ibrahim, S.A. Kalsbeck, R.S. Little, S. Malla, Howard J. Woodard, Anthony Bly, Ron Gelderman, Jim Gerwing, and Gary Erickson (South Dakota State University); and L. Hesler, W. Riedell, and S. Osborne (USDA-ARS-GIRL).

Winter wheat breeding and genetics.

A.M.H. Ibrahim, S.A. Kalsbeck, R.S. Little, and S. Malla.

Crop Report and Testing Sites. Winter wheat production in 2003 was estimated at 59.34 million bushels, up 227 % from last years drought-impacted production and is the third largest production in the state's history. Producers harvested 1.38 million acres (1.6 million planted acres), for a state average of 43 bu/acre, which is 14 bushels above last year's and is the second highest yield in the state's history. Overall, the excellent winter survival rate at most locations was due to a mild winter and further aided by an early mild spring with adequate rainfall.

In 2003, the winter wheat breeding program conducted testing at eight sites throughout South Dakota. These environments included Aurora and Brookings (Brookings Co.), Platte (Douglas Co.), Highmore (Hyde Co.), Selby (Walworth Co.), Winner (Tripp Co.), Wall (Pennington Co.), the Northeast Research Farm near Watertown (Codington Co.), Kennebec (Lyman Co.), and both irrigated and dry land environments at the Dakota Lakes Research Farm east of Pierre (Hughes Co.). Crop performance testing also was conducted at an additional nine sites west of the Missouri River

in cooperation with Bruce Swan and John Rickertson (SDSU West River Agricultural Research and Extension Center, Rapid City).

Autumn stand establishment at most testing locations was average. Late planting at Selby and the Northeast Experiment Station resulted in limited plant development and were abandoned in the spring. Extreme drought and cropping history lead to the abandonment of the dry land nursery at Dakota Lakes. Limited subsoil moisture at all west river locations was aided by May and June temperatures that were 4–5°F below normal and supplemented by above normal rainfall. Plants produced very few tillers at the Central Crops and Soils Research Station in Highmore but compensated by good grain filling aided by a mid-June rainfall. Conversely, plants in the nurseries at Wall and Winner had excellent plant tillering but less than average grain yield due to poor grain filling caused by limited post-anthesis moisture. At Platte, Brookings, and Kennebec, yield and test weight was above the 3-year average due to timely rainfall during plant development. One experimental variety yielded 99 bu/acre at Brookings

Foundation Seed Increase. Two lines are being increased for foundation seed.

SD97W604 (SD89333, Gent/Siouxland//Abilene) is a HWWW with high yield potential, early maturity, and excellent noodle quality. SD97W604 ranked at the top in 2003 South Dakota Crop Performance Testing (CPT) Variety Trial. SD97W604 ranked above all available HWWW lines in 4-year grain yield average, Polyphenol Oxidase (PPO) enzyme levels, and winter survival ability. SD97W604 has exhibited moderate adult-plant and seedling resistance to prevalent races of stem rust and has been postulated to carry *Sr24* and *Sr31* genes based on tests conducted by the USDA Cereal Disease Laboratory, St. Paul, MN. In tests done in the greenhouse at South Dakota State University, SD97W604 has exhibited resistance to RCR and was moderately resistant to TPMK and bulk mixture of stem rust races. SD97W604 is moderately resistant to field leaf rust and is tolerant to tan spot. SD97W604 was tested in 1999 in cooperative baking tests conducted by the USDA/ARS Hard Winter Wheat Quality Lab (HWWQL). Baking scores were poor. The T1BL·1RS rye translocation in SD97W604, which confers disease resistance, also is responsible for poor baking quality, confirmed by 4 years of predictive sedimentation tests and mixograph tests from two locations. Protein levels for SD97W604 have ranged from well above average to well below average in four years of testing. SD97W604 has low PPO levels, which is essential for good noodle quality, an attribute desired of HWWW cultivars. Flour yield of SD97W604 is above average. Results of noodle-making tests indicate that SD97W604 possess excellent noodle quality. SD97W604 has a short coleoptile, a trait typical of most of the experimental and released white wheat currently available. As breeding for white wheat in South Dakota progresses, lines with longer coleoptiles will be selected and advanced. SD97W604 has fair to good resistance to preharvest sprouting and will be best adapted to west of the Missouri river environments. SD97W604 is on large-scale increase with intention to release in 2004.

SD92107-5 (Brule//Bennett/Chisholm/3/Arapahoe) is a reselection from the cultivar Harding for better yielding ability and test weight. This line significantly yielded better than its sibling Harding in the last 4 years of CPT testing, and has a good disease package similar to it. However, SD92107-5 possesses better resistance to stem rust races than Harding. SD92107-5 is targeted for production systems where the potential for winter injury is of greatest concern, especially in the northern half of the state and conventional summer fallow production systems (with minimal or no crop residue at planting) across South Dakota. Across locations and years, SD92107-5 has shown superior performance in situations where winter injury has been an important factor in yield rankings and has shown good yield performance compared to other winter-hardy varieties after a mild winter. SD92107-5 has very good baking quality, similar to its sibling, and has better test weight. SD92107-5 will be purified this year with intention to increase in 2004 and release in 2005.

Fusarium head blight. We made significant progress in evaluating germ plasm and developing segregating populations that possess enhanced scab resistance. We have been evaluating elite breeding lines, introduced germ plasm, regional nurseries, commercial cultivars, and segregating populations in our mist-irrigated scab nursery since 1999. Approximately 6000 plants were evaluated for scab resistance during the 1999 season. One-thousand five hundred of the plants were kept and were planted into the field in 2000 (as $F_{3,4}$ progeny rows). Forty-four lines were selected out of 1,500 based on agronomic performance and were planted in 2001–02 season in the early yield trial nursery (as $F_{3,5}$ lines). These lines also were planted in the greenhouse to confirm resistance. Heads were also picked from the best promising $F_{3,4}$ progeny rows and planted in the mist-irrigated nursery to obtain scab reaction data prior to line entry in the preliminary yield trials the following year. In the 2001–02 growing season, we planted 3,631 progeny rows, with resistant sources, under normal winter wheat production practices in Dakota Lakes, SD. These progeny rows were planted in spring wheat stubble with supplementary irrigation. The best 291 lines were advanced to the $F_{3,5}$ yield trials and observa-

tion rows of these were evaluated in the mist-irrigated nurseries in the field and greenhouse in 2003. We have used marker-assisted selection (in collaboration with Yang Yen, SDSU Molecular Biologist) as a complementary tool to our traditional breeding methods, to evaluate resistance in our promising advanced generations (AYT and CPT).

We investigated planting schemes between 2001 and 2003 to determine if direct seeded row materials are affected differently than transplanted hill plots when they are inoculated with FHB. Preliminary results suggested that there were indeed significant correlations between the two methods. We also started using point inoculation to evaluate winter wheat lines and varieties for scab tolerance under greenhouse conditions in 2002.

Mr. Subas Malla joined our program in the autumn of 2002 to pursue and M.S. degree. He is assisting with the breeding program and conducting independent research regarding the genetics of scab resistance in hard winter wheat germ plasm.

White wheat. In previous years, our breeding efforts for HWWW have centered on making crosses between adapted red lines and unadapted white germ plasm. We incorporated resistance to prevalent races of stem rust and increased the winter survival ability of HWWW. We also increased coleoptile length of our HWWW germ plasm and decreased PPO activity (a predictive measure of noodle-making quality) without sacrificing bread-making qualities. In 2003, for both red and white germ plasm in advanced nurseries, we increased coleoptile length by an average of 1 cm. The percentage of white lines (40 %) with coleoptiles longer than the cultivar Harding was twice that of red lines (20 %) in 2003 advanced nurseries (the coleoptile length of Harding is considered to be a standard for acceptable emergence following deep planting). In 2004, few of the long coleoptile lines were advanced to the AYT nursery with the result that only 2 of 7 white lines and 3 of 36 red lines had coleoptiles at least as long as Harding. However, in the 2004 preliminary yield trial (PYT) nursery, 40 % of both red and white lines had coleoptiles at least as long as Harding. Preharvest sprouting resistance is one of our biggest challenges and commands our intense effort. Nuplains and Trego, the only two elite HWWW cultivars with acceptable adaptation for some environments in South Dakota, have been identified as very good lines for sprouting resistance. Of the tested experimental lines entered into 2003 and 2004 advanced nurseries, 96L9643-3 rated very good both years; SD97W671-1 rated good in 2003 and fair to good in 2004; and SD97W604 (2004 potential release) and SD00W087 rated fair to good both years. Of other experimental lines entered into 2004 advanced nurseries, nine SD01W lines as well as SD97W609 (2004 potential release), SD97W604-1 and SD99W015 rated very good for sprouting tolerance. The headrow nursery in Dakota Lakes Research Farm consisted of 3,933 white progenies in 1998, 5,340 in 1999, 1,635 in 2000, 7,502 in 2001, 1,954 in 2002, 11,707 in 2003, and 4,915 in 2004. The early yield trial (EYT) nursery had 125 HWWW entries in 1998, 182 in 1999, 174 in 2000, 117 in 2001, 99 in 2002, 141 in 2003, and 270 in 2004. The PYT nursery had 44 HWWW entries in 1999 and 2000, 40 in 2001, 26 in 2002, 29 in 2003, and 39 in 2004. The AYT nursery had 3 experimental HWWW entries in 1998, 26 in 1999, 22 in 2000, 10 in 2001, 11 in 2002, 14 in 2003 and 8 in 2004. The CPT nursery had 3 experimental HWWW entries in 2000 and 2001, 5 in 2002, 4 in 2003 and 5 in 2004. The number of white samples examined in routine quality tests more than doubled from 1998 to 2003. Tests included protein, test weight, computerized mixographs, sedimentation, PPO activity, sprouting tolerance, and coleoptile length in addition to seedling stem rust, and field WSMV and scab screening. Two lines, SD97W604 (SD89333 (Gent/Siouxland//Abilene) and SD97W609 (Abilene/Karl), are on foundation and breeder seed increase, respectively, with potential release in 2004 and 2006, respectively.

Development of combined meal PPO and sedimentation test for HWWW. We developed a protocol that simultaneously measures meal sedimentation and PPO activity for early generation quality screening during the short turnaround period between harvest and planting. Our regular sedimentation tests were usually conducted with 1 gram of ground meal from a 10-gram sample to predict gluten strength, whereas our PPO assay (predictive measure of noodle discoloration) was conducted with five whole-seed samples. A final combined protocol was selected based on correlations with standard tests for sedimentation, PPO, and computerized mixograph data. The combined protocol was built on the meal SDS-sedimentation protocol, with adjustments in temperature, MOPS (3-(N-Morpholino) propane-sulfonic acid) buffer concentration, lactic acid concentration, and the timing of steps. In this combined protocol, 4 ml of 10 mM L-DOPA (L-3,4-dihydroxyphenyl alanine) replaced 4 ml of water, whereas various levels of lactic acid were tested. PPO color development improved with time and was acceptable at 42 minutes. Use of the most promising combined protocol (5 ml lactic acid, 4 mL 10 mM L-DOPA in 150 mM MOPS buffer, with ambient temperature of 24°C. and measurement of sedimentation at 41 min and color at 42 min) provided acceptable PPO and sedimentation scores. The stability (CV% = 12.8) of PPO values in the combined protocol was greatly improved compared to that (CV% = 22.3 %) of the 5-grain visual PPO test. The stability of the sedimentation portion (CV% = 3.4) of the combined protocol matched that of the

standard meal sedimentation test ($CV\% = 4.5$). Both sedimentation tests were highly correlated with mixograph scores loading on a factor associated mainly with mixing tolerance. Highly skewed results for meal PPO and sedimentation obscured distinctions among higher values. All protocols (standard or new) produced highly significant location-by-entry interactions, indicating a need to test over multiple environments before using data for screening purposes. Further tests will be conducted on seed harvested from 2005 Advanced Yield Trials to confirm the repeatability of the combined protocol.

Cereal aphids and other arthropods.

L. Hesler, W. Riedell, and S. Osborne (USDA-ARS-NGIRL).

Research continues on ways to limit infestations of cereal aphids, other arthropod pests, and diseases in wheat. We are determining the mechanisms and levels of resistance to bird cherry-oat aphids among wheat and related grasses. We are also evaluating how agronomic practices affect infestations of cereal aphids and other insects. For instance, with Dr. Robert Berg, SDSU Southeast Research Farm, we found that spring cereals grown under minimum tillage have greater infestations of bird cherry-oat aphid than under conventional tillage. With Dr. Marie Langham (SDSU, plant virologist), we are determining how planting date of wheat affects insect infestations, incidence of viral diseases, and plant growth and yield. We also are collaborating with Dean Kindler and Norman Elliott (USDA-ARS-PSWCRL, Stillwater, OK) to develop rearing methods, determine host plant suitability, and characterize plant damage by the rice root aphid, another member of the cereal aphid complex and vector of BYDV.

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Crop nutrition management of hard red winter and hard red spring wheat in eastern South Dakota.

Howard J. Woodard, Anthony Bly, Ron Gelderman, Jim Gerwing, and Gary Erickson.

Crop Rotation, tillage method, and crop residue management study at Brookings, SD. A site located on the Old Larsen Farm near Brookings was selected for the rotation study. The soil type at this site is the Divide series. Plots were established in August 1999. Crop rotations established in 2000 were corn/soybean, spring wheat/soybean, and corn/soybean/spring wheat. No-till and conventional tillage blocks were established for each crop rotation. Conventional tillage plots were tilled with a disk/chisel plow and leveled with a disk in November and April, respectively. Residue management plots were included in the plot design for each crop rotation and tillage system as either completely removing all loose residues (residue removal) or leaving the residues in place (residue maintenance). In the residue removal plots all of the loose residues across the whole plot were removed. The plot design is a strip-split-split randomized complete block with four replications. Plot size is 30' x 30'. Preplant, composite soil samples were taken from each replication for nutrient recommendations.

Oxen HRSW was seeded at 1.2 million pure live seeds on 10 April, 2003. Nitrogen fertilizer (70 lbs/acre) as urea and chloride (40 lbs/acre) as KCl was broadcast applied to the wheat plots on 23 April, 2003. Corn (Dekalb 4446 RRBt) was planted at 28,800 seeds/acre on 28 April, 2003. Nitrogen (reps 1 and 2 = 100 lbs/acre, and reps 3 and 4 = 38 lbs/acre) was broadcast applied as urea to corn plots on 3 June, 2003. Sulfur (10 lbs/acre) was broadcast applied to reps 1 and 2 corn plots as gypsum on 3 June, 2003. Spring wheat was sprayed with Puma (7 oz/acre), Buctril (1 pt/acre), and MCPA Ester (1.25 oz/acre) on 23 May, 2003, for weed control. Spring wheat was harvested on 13 August, 2003, with a plot combine. Wheat straw was gathered from a 125 ft² subsection of each plot, weighed and a subsample obtained for

nutrient analysis. Straw was returned to the residue maintenance plots and removed from the residue removal plots on August 15, 2003. Grain test weight and crude protein was measured by standard NIR techniques. Dependent variable statistics were computed with SAS.

Statistical analysis of data was performed for each crop. Analysis by tillage method and residue management was performed. ANOVA showed that no treatment or interaction significantly influenced grain yield or protein. Statistical analysis by tillage system or residue maintenance showed no significant influences with either residue management treatment or tillage method. Tillage method significantly influenced residue weight (Table 1). No-till had higher residue weight. Statistical analysis by residue maintenance showed that where residues are maintained on the plot that no-till had significantly higher residue dry matter weights. When residues are removed there is no significant difference between tillage systems. Overall spring wheat grain yields were very good.

Comparison of liquid and dry nitrogen fertilizer materials influence on grain protein and yield of hard red spring wheat at Brookings, SD. Increases in grain protein from applications of foliar N have been reported. Postpollination applications have been shown to be the most effective. Some researchers have said that broadcast application of dry fertilizers would be more effective than liquids because it is root uptake that is responsible for getting N into the plant. They say that foliar N applications are washed off and subsequently taken up by the roots anyway. Therefore, a research project was initiated to evaluate the influence of dry and liquid forms of UAN (urea ammonium nitrate) and AMN (ammonium nitrate) fertilizers applied after pollination on hard red spring wheat grain protein and yield.

A research site on the Agronomy research farm near Brookings, SD was selected. This site had been fallowed for three years. A combination of tillage and Roundup had been used on this site for weed control. A composite of 15 preplant soil samples from 0–6 and 6–24 inch depths were taken prior to planting to evaluate soil nutrient status. The Oxen HRSW was no-till seeded in 7-in rows at 1.2 million pure live seeds/a on 10 April, 2003. Nitrogen fertilizer (70 lbs/a) as urea and chloride (45 lbs/a) as KCl (0-0-60-45 Cl) was broadcast on all plots after planting. Plot width was 5 feet and length 25 feet. All plots were sprayed with Buctril (1 pt/acre), Puma (7 oz/acre), and MCPA ester (1.25 oz/acre) on 23 May, 2003 for broadleaf and grass weed control. An adequate number of plots were established to accommodate five treatments in four replications. The five treatments were a check, dry or liquid ammonium nitrate (AMN) and dry or liquid urea ammonium nitrate (UAN).

The treatment applications were applied after pollination at 30 lbs N/acre. Liquid UAN and dry AMN are common fertilizer materials. However, dry UAN and liquid AMN are not. To get dry UAN, common urea and ammonium nitrate fertilizers were used. This mixture is quite hydrophilic, therefore the usability of mixing them was not feasible. The correct amounts of urea and ammonium nitrate were calculated to represent the proportions in liquid UAN. The urea and ammonium nitrate were weighed and applied separately to each plot by hand. Dissolving the correct amount of AMN in water easily created liquid AMN. The rate of application for both liquid fertilizer materials was 20 gpa. The liquid UAN solution was a 1:1 blend with water. The dry and liquid fertilizer treatments were applied on 3 July, 2003. Precipitation is monitored at the Agronomy farm by standard weather service equipment. Rain was received 1 and 6 days after treatment application (0.16 and 1.13 inches, respectively). There should have been plenty of time for the foliar treatment applications to be absorbed by plant foliage since the rain 1 day after application was small as well as enough rain 6 days later to incorporate the dry fertilizer into the soil for root absorption. Grain was harvest from the plots with a small-plot combine on 8 August, 2003. Grain weight was recorded for yield calculations and a subsample retained for test weight, kernel weight, and grain protein determination. Dependent variable statistics were evaluated with SAS.

Plant stand and growth was excellent due to very good growing conditions. Composite soil test results from a two-foot sampling depth showed that nitrate levels were 108 lbs/acre, sulfur levels were 58 lbs/acre, and there was only 16 lbs/acre chloride available. Six inch soil test for Olsen P was 24 ppm (very high), extractable K was 840 ppm (very high), and pH was 6.4. ANOVA of dependent variables showed that treatment did not significantly influenced grain protein, test weight, yield, or kernel weight. Grain yield was very good and was between 61 and 65 bu/acre for all treatments. Grain protein was very high and probably due to an over supply of nitrogen. The grain yield was good but not enough for the 108 and 70 lbs of N that was available from soil test and fertilizer N application. Orthogonal contrasts for grain yield did not show any significant results for the comparisons made, however there were significant results for grain protein. The liquid N fertilizer materials (mean = 16.3 %) significantly increased grain protein in comparison the check (mean = 15.6) and the dry fertilizer materials (mean = 15.9). These results are very similar to what was concluded from 2001 and 2002 data.

This data would suggest that plant tissues are absorbing N from foliar applications of liquid fertilizer materials and not being washed off and taken up by the roots. The liquid UAN fertilizer material significantly increased grain protein when compared to the check and other dry fertilizer materials.

Nitrogen application timing and rate influence on HRSW grain protein and yield near Aurora, SD, in 2003. The nitrogen requirement for spring wheat is estimated at 2.5 lbs N/bu grain. If the spring wheat plant does not have access to N by a specific growth stage, grain yield reductions will occur. A recent management trend in the upper Great Plains for spring wheat has been to apply N at many different growth stages. This trend has come from Europe where the grain-fill period is much longer than in South Dakota and is known as 'spoon feeding.' Because our growing season and grain-filling period is much shorter than for Europe, a research study was initiated to measure the influence of N application timing on HRSW grain yield and protein.

A research site near Aurora, SD, was selected that had been under no-till since 1993. The prior crop was soybeans and rotated with corn since 1993. Composite soil samples from the 0–6 and 6–24-in soil depths were taken prior to planting for nutrient analysis. Five application timings for nitrogen were used that included planting, tillering, jointing, boot, and heading growth stages. The N application rate was kept low (50 lbs/acre) as to not over estimate N requirement of the plants and therefore overshadow any treatment differences. A control and high N rate (100 lbs/acre) were also included in the treatments. The nitrogen was applied as broadcast ammonium nitrate. Oxen hard red spring wheat was no-till planted on 14 April, 2003, at 1.2 million pure live seeds/acre. At planting, 75 lbs P_2O_5 as 0-46-0 was applied with the seed in 7-in rows. Sulfur (21 lbs/acre) was applied to all plots on 1 May, 2003, as broadcast gypsum. The N application timings were applied on 6 May (tillering), 9 June, (jointing), 16 June (boot), and 26 June (heading). Weeds were controlled with Buctril (1 pt/acre), Puma (7 oz/acre), and MCPA ester (1.25 oz/acre) and applied on 23 May, 2003. Plots were harvested with a small plot combine on 1 August, 2003. After harvest, 0–24 inch soil samples were taken for residual NO_3-N analysis. Grain protein was measured with near-infrared reflectance. Dependent variable statistics were determined with SAS.

Soil test results (0–6") showed 3.5 % organic matter, 23 ppm Olsen P, 211 ppm extractable K, and 0.3 mmho/cm salts. Soil test results (0–24") showed 16 lbs/acre NO_3-N , 32 lbs SO_4-S , and 284 lbs/acre Chloride. N application timing significantly influenced grain protein and yield (Table 1). The N applied at planting and tillering had the highest grain yield. As N was applied later in the growing season, yield was significantly reduced. Grain protein was the highest with treatments that yielded the lowest except the check plot which did not have enough N for yield or protein (Table 1). Typically, the highest grain yielding wheat has the lowest protein except when an abundance of N is available. The high N rate (100 lbs N/acre) did not have the lowest protein because only six more bushels of grain were gained from the addition of 50 lbs N/acre resulting in a sufficient amount of N available for protein which was similar to lower yielding treatments. N rate significantly increased grain yield (0, 50, and 100 lbs N/acre, yielded 47, 70, and 76 bu/acre respectively). A very good relationship occurred between grain yield and protein for the N timing applications (Figure 2). Late N application was not available for dry matter accumulation but was available for increasing the N (protein) content of the grain.

Sulfur influence on spring wheat at Aurora, SD. Crop sulfur (S) deficiencies have increased in the past years. Many corn fields have shown S deficiencies. Soybeans have rarely been S deficient. There is little work with S and spring wheat. Therefore a research project was initiated to investigate whether spring wheat would respond to S application.

A research site near Aurora, SD, was chosen that had a low S soil test. A RCB design with two treatments was used. The treatments were either with or without S application. The S-treated plot received 25 lbs S/acre as gypsum, which was surface broadcast after planting the spring wheat. Nitrogen fertilizer (90 lbs/acre) was applied to all plots as surface broadcast ammonium nitrate after planting. Oxen spring wheat variety was no-till planted on 14 April, 2003, at 1.2 million pure live seeds/acre in 7-in rows. Phosphorus (75 lbs/acre) was applied with the seed as 0-46-0. Weed control was accomplished by spraying all plots with Buctril (1 pt/acre), Puma (7 oz/acre), and MCPA ester (1.25 oz/acre) on 23 May, 2003. Grain was harvested with a small plot combine on 1 August, 2003. Grain yield statistics were completed with SAS. Postharvest soil samples (0–24 in) were obtained for NO_3-N and SO_4-S analysis.

Sulfur did not significantly influence spring wheat grain yield. Yields were very good. A yield increase to sulfur was expected since the preplant SO_4-S soil test (0–24 in) was only 14 lbs/acre. Postharvest soil test analysis showed equal amounts of NO_3-N and SO_4-S in the 0–24-in soil layer for each treatment.

Managing cultural practices for high yield wheat in northeast South Dakota. Many cultural practices are available to growers that under certain circumstances, increase wheat yield. Some individuals have recommended using many of these practices together to attain higher wheat yield. Often, the use of such practices would not be recommended by standard agronomic principles. These individuals claim that the combined use of these practices will result in higher wheat yield. Due to this theory, a research project was conducted to determine the combined and individual effect of several cultural practices for increased wheat grain yield.

A research site was selected on the Northeast Research Farm near South Shore, SD. The soil type is a nearly level silty clay loam soil (Brookings) that is common to North East South Dakota. Composite soil samples of the 0–6 and 6–24 inch depths were obtained during the autumn of 2002 and analyzed for nitrate-nitrogen, phosphorus (Olsen method), potassium, pH, organic matter, salts, zinc, sulfur, manganese, copper, chloride, calcium, and magnesium. The five cultural practices chosen for evaluation were soil fertility with a sulfur comparison, split application of nitrogen, seeding rate, foliar fungicide, and fungicide seed treatment. The five cultural practices were employed to compare with standard recommended methods for successful wheat production. The soil fertility comparison was made between standard nutrient recommendations determined from soil test results for a 60 bu/acre yield goal and nutrient applications for 100 bu/acre yield goal. The split application of nitrogen was evaluated by splitting the N for the 100 bu/acre yield goal into 3 timings, planting, tillering and boot growth stages. The standard seeding rate of 1.2 million pure live seeds (PLS)/a was compared to 2.2 million PLS/acre. Applying 4 oz/acre Tilt at flag leaf and 4 oz/acre Folicur at heading was the treatment used for disease control. The fungicide seed treatment used was Raxil XT (0.16 oz/100 lbs seed). The treatments used to test these cultural practices were determined so that comparisons of each practice with an appropriate check could be made as well as the combined effect of all the practices. Treatments were randomized in a complete block design with four replications. The fertility comparison treatments were split in each block with filler plots to minimize any border effect from the high N rate applied for the 100 bu/acre yield goal.

Ingot HRSW was no-till planted on 8 April, 2003, into soybean residue. All plots were sprayed with a herbicide tank mix of Puma (7 oz/acre), Buctril (1pt/acre), and MCPA Ester (1.25 oz/acre) on 23 May, 2003. Weed control was excellent. The second and third nitrogen application splits were applied on 23 May and 11 June, respectively. Tilt (4 oz/acre) and Folicur (4 oz/acre) were applied on 11 June and 1 July, respectively. Plots measured '5 x 15' feet and were harvested with a small plot combine on 31 July, 2003. Grain protein was determined with standard NIR technique. Grain yield and protein were adjusted to 13 % grain moisture. Mean determination and separation was accomplished with SAS. Orthogonal contrasts for each cultural practice were performed to determine if the individual practice had an effect on the measured parameter.

Preplant soil test analysis showed that nitrate-nitrogen was limiting for both the 60 and 100 bu/acre yield goals. Nitrogen was applied at a rate of 85 lbs/acre and 185 lbs/acre as urea for the recommended and maximum soil fertility treatments, respectively.

Phosphorus (P) was in the high (14 ppm) category and therefore no P was applied to the recommended plots, but 30 lbs/acre P_2O_5 was applied with the seed as 0–46–0 to the maximum soil fertility treatments. Potassium (K) was also in the very high (187 ppm) category and none would have been recommended. However since there was only 10 lbs/a chloride (Cl^-) in the top two feet, 38 lbs/acre Cl^- was applied to both the recommended and maximum soil fertility treatments. This Cl^- application resulted in 50 lbs/acre K applied to all plots. Soil pH was 6.3 and salts were 0.3 mmho/cm. Zinc was in the medium category (0.54 ppm). Since wheat has not been shown to respond to zinc application, none was applied to the recommended treatment plots. Zinc was applied to the maximum soil fertility plots at 0.5 lbs/acre with the seed as zinc sulfate. The sulfur test showed 18 lbs/acre in the top 2 feet. Sulfur was applied to the recommended soil fertility plots, but another recommended soil fertility treatment was added that had no sulfur application. Sulfur at 56 lbs/acre was applied to the maximum soil fertility plots as gypsum (calcium sulfate). This gypsum application also resulted in 69 lbs/acre calcium applied to the maximum soil fertility plots. The calcium soil test was considered very high (2,798 ppm) and, therefore, none was applied to the recommended soil fertility plots. Manganese and copper were considered high (36.5 and 0.89 ppm, respectively) and therefore none was applied to the recommended soil fertility plots but 2 lbs/acre and 0.5 lbs/acre manganese and copper respectively were applied with the seed in the maximum soil fertility plots as the sulfate form. Magnesium was very high and none was applied to the recommended soil fertility plots or maximum soil fertility plots because individuals recommending practices for high yield wheat say that magnesium levels are already too high and calcium should be applied as gypsum to balance the high magnesium.

There was a significant treatment effect on grain yield, which ranged from 41.7 to 53.2 bu/acre. Twelve treatments make it hard to distinguish what is happening so orthogonal comparisons were used to separate meaningful treatment comparisons. Grain test weight was significantly higher for the recommended soil fertility treatment plots when compared to the maximum soil fertility treatment plots. Grain protein was significantly higher for the maximum soil fertility treatments plots when compared to the recommended soil fertility plots because of the extra nitrogen that was applied. The check plot without nitrogen had significantly lower protein when compared to the maximum and recommended fertility treatment plots.

Orthogonal contrasts for soil fertility treatment showed that grain test weight was significantly higher with the recommended treatments, grain protein was higher for the maximum treatments and grain yield was not different. Seeding rate and foliar fungicide application significantly influenced grain test weight, protein and yield. However, the differences between the seeding rate and fungicide treatments for grain test weight and protein are really insignificant when considering any price dividends that could be received. Increasing the seeding rate from 1.2 to 2.2 million seeds/acre decreased the grain yield 4 bu/acre. Applying foliar fungicide increased yield 4.8 bu/acre. Split N application did not significantly influence any of the dependent variables. Sulfur application significantly decreased grain test weight, had no effect on protein and significantly increased grain yield. The sulfur application seemed to decrease grain test weight only because we see that as yield increases, grain test weight decreases.

Soil fertility and testing studies on spring wheat and corn in Brown County, South Dakota. Evaluating and improving soil test recommendations is important and constantly needed to provide farmers with accurate and up to date information. Farmers are getting recommendations from many sources with little or no knowledge of product success. Crop sulfur deficiencies have been more common in South Dakota during the last few years, especially with no-till. Gypsum has been promoted to balance the ratio of calcium and magnesium by outside salesman. Therefore, several studies were initiated to evaluate the influence of chloride, sulfur, and gypsum application on spring wheat and phosphorus, sulfur and gypsum application on corn in Brown Co, SD.

Two sites each for spring wheat and corn were located in farmer fields. Nutrient treatments were surface broadcast applied after the farmers planted and applied their planned fertilizer applications. Conventional tillage was used on sites 1 and 2, strip tillage on site 3 and no-till on site 4. The farmers did not apply the nutrients evaluated with these projects except for nitrogen. Nitrogen was applied to all treatment plots to offset the nitrogen applied with the ammonium sulfate treatment. Sulfur was applied as ammonium sulfate (NH_4SO_4) (21-0-0-24), chloride as potash (0-0-60), and phosphorus as triple super phosphate (0-46-0). Gypsum is calcium sulfate (CaSO_4) and contains 18 % sulfur and 23 % calcium by weight. Plot dimensions were '20 x 20' feet. Composite soil samples from the 0-6 and 6-24 inch soil depths were obtained from the research area for nutrient analysis. Grain yield was determined from hand harvesting 25 and 100 ft² from each spring wheat and corn plot, respectively. Statistics were determined with SAS.

Chloride, sulfur, and gypsum application did not significantly influence grain yield, protein or test weight at site 1. Grain yield was very good. Sulfur application did not significantly influence grain yield at site 2. Grain protein and test weight was significantly lower with sulfur application at this site. Grain yield was lower than average because of heavy foxtail pressure. Phosphorus, sulfur, or gypsum application did not significantly influence corn yield at sites 3 or 4. A check of the farmer's corn yield at site 3 also verified that further nutrient applications did not significantly improve grain yield. Sites 2 and 4 had the lowest sulfur soil test and should have shown a grain yield response to sulfur application. Yields were higher with sulfur application at sites 2 and 4 but could not be determined to be significantly different from plots without sulfur application. Additional nitrogen application at sites 1, 2, and 4 above the farmer's applied rate did not significantly increase grain yield, which indicates that the farmer's applied rate did not limit crop productivity.

ITEMS FROM UTAH

USDA–ARS FORAGE & RANGE RESEARCH LABORATORY
Utah State University, Logan, UT 84322-6300, U.S.A.
<http://www.usu.edu/forage/frrl.htm>

Newly released salt-tolerant wheat germ plasm lines are useful in gene pyramiding.

Richard R.-C. Wang.

Two salt-tolerant wheat germ plasm lines, **W4909** and **W4910**, were jointly released by USDA–ARS and Utah Agricultural Experiment Station in 2002. The lines have been registered in Crop Science as GP-730 and GP-731, PI 631164 and PI 631165, respectively.

W4909 and W4910 had been compared to the known salt-tolerant cultivars Kharchia 65, KRL 1-4, KRL 19, Lu 26S, and Shorawaki in a 2003 greenhouse experiments. Both W4909 and W4910 are equal to Shorawaki in survival after salinity treatment at EC = 42 dS/m, whereas all the other lines had lower survival rates. At the end of the salinity treatment, W4909 and W4910 had more tillers than Shorawaki. After being moved to potting medium without salt solution, W4909 and W4910 produced more seeds/spike than Shorawaki. W4910 had the highest number of spikes/plant, followed by Shorawaki and W4909.

The F₃ families of ‘Yecora Rojo/W4909’ and ‘Yecora Rojo/W4910’ exhibited transgression segregation for salt-tolerance and agronomic traits. W4909 and W4910 were found to have salt tolerance mechanisms other than NaCl exclusion. Therefore, we can enhance salt tolerance by gene pyramiding with crosses of W4909 or W4910 and other salt-tolerant wheat cultivars having NaCl avoidance as the mechanism.

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VIRGINIA**VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY****Department of Crop and Soil Environmental Sciences, Blacksburg, VA 24061, U.S.A.**

J.J. Paling, C.A. Griffey, W.E. Thomason, J. Chen, J.A. Wilson, D. Nabati, T.H. Pridgen, E.G. Rucker, D.E. Brann, and M.M. Alley.

2003 Wheat Production in the Commonwealth of Virginia.

J.J. Paling, C.A. Griffey, W.E. Thomason, D.E. Brann, and M.M. Alley.

Growing conditions. Producers began planting into dry soil during autumn 2002 hoping for some moisture later, but the dry conditions that prevailed during most of 2002 changed mid way through the planting season. Autumn rains turned the dry conditions into extremely wet conditions and delayed some wheat planting until much later than usual with only 76 % of the crop planted by 16 November. These unusually wet conditions continued through the winter, and temperatures were lower than average for much of the state. Cool and wet conditions continued through April and May. Many farmers proclaimed the spring of 2003 as 'the wettest spring I can remember' and, indeed, it was one of the wettest years on record. These cool wet conditions remained through harvest season, delaying wheat maturity and harvest by 1 to 2 weeks.

Disease incidence and severity. Powdery mildew incidence was lower and occurred later than usual in the Eastern Shore and Coastal Plain regions. Above average rainfall and colder than average temperatures, during the time when powdery mildew epidemics usually occur, likely delayed onset and spread of this disease. Leaf rust incidence was lower in 2003 than in 2002 over most of the state. Trace amounts of stripe rust were observed on the Eastern Shore in 2003. Lodging was most severe in areas having heavy disease during the wet spring. Reports of diseased wheat fields lodging from the wet conditions began as early as mid May. Diseases of major significance in 2003 were scab and glume blotch, which thrived under the wet conditions that occurred during heading and grain fill. These two diseases resulted in significant losses in grain yield and quality, and most grain was unsuitable for milling purposes. The 2003 season highlighted the importance of integrated pest management including planting disease resistant cultivars, treating seed, and using IPM control measures.

Insects. The cereal leaf beetle was the most prevalent insect reported in 2003. Scouting reports of insect incidence and severity were accompanied by recommendations for control. The beetle reached economic threshold and control was necessary in several fields in eastern Virginia.

State cultivar tests. During the past two seasons, the environment in Virginia has facilitated the evaluation of daylength sensitivity, spring freeze damage, resistance to glume blotch, FHB, and overall plant health in both a dry (2002) and an excessively wet years (2003). Newer wheat cultivars and lines performed well in both of these test environments. A total of 71 entries were evaluated at five locations across the Commonwealth in 2003. Included in this total were 41 experimental lines (32 developed at Virginia Tech) and 30 released cultivars. Average grain yields ranged from 42 to 77 bu/acre (2,822–5,174 kg/ha) with an overall test average of 63 bu/acre (4,233 kg/ha). Wheat cultivars with yields significantly above the test average included SS 520, Tribute, SS 550, Sisson, McCormick, Renwood 3706, SS 560, and 16 experimental lines (12 from the Virginia Tech program, including two soft white-entries). Yields among genotypes in this group ranged from 66 to 77 bu/acre (4,434–5,174 kg/ha). Tests conducted in the Coastal Plain Region had a yield average of 64 bu/acre (4,300 kg/ha), whereas tests conducted in the Piedmont and Blue Ridge Region had a yield average of 62 bu/acre (4,166 kg/ha). Test weights of wheat lines (based on five locations across the state) ranged from 49.6 lb/bu (638 kg/m³) to 57.6 lb/bu (741 kg/m³) with a test average of 54.4 lb/bu (700 kg/m³). Of the 24 entries with test weights significantly higher than the test average, 11 were released cultivars and 13 were experimental lines. Five cultivars, McCormick, Renwood 3706, Sisson, SS 520 and Tribute, and six Virginia experimental lines, had both grain yields and test weights that were significantly higher than the test average.

Virginia no-till test. To evaluate cultivar by tillage effects, wheat was planted into corn stubble at the Eastern Virginia

AREC near Warsaw, VA, on 23 October. Grain yields averaged 85 bu/acre (5,711 kg/ha) with an average test weight of 57 lb/bu (733 kg/m³). The top yielding cultivars produced more than 90 bu/acre (6,047 kg/ha) in 2003. Cultivars with moderate resistance to FHB were among the highest yielding during the past 3 years and included two new releases, McCormick and Tribute, each yielding significantly higher than the test average in all 3 years. Improved scab resistance will increase the productivity of growing wheat especially in no-till management regimes following corn.

Virginia wheat yield contests. Seven official entries were in the 2003 wheat yield contests and three additional entries were submitted for informational purposes. Three of the entries were grown in no-till and the other four entries in conventional-till regimes. In general, yields for the entries in 2003 were lower than in 2002, likely due to the wet conditions that occurred throughout much of the growing and harvesting seasons. The highest yield in no-till was obtained by George Floyd III of Northampton County. He produced 97 bu/acre (6,517 kg/ha) of Century II wheat after soybeans. George Alvis and George, Randy, and Dennis Alvis (Alvis Farms) of Hanover County had the other two no-till entries. Each of these fields of SS 520 yielded 77 bu/acre (5,174 kg/ha) after corn. Richard T. Sanford of Westmoreland County had the highest yield under conventional tillage. His field of SS 550 produced 80 bu/acre (5,375 kg/ha) grown after a previous crop of barley/soybeans. Joseph Reamey of Montross in Westmoreland County submitted two entries, one field of Sisson and a field of Vigoro 9110. Each field was grown after corn and produced 53 bu/acre (3,561 kg/ha). Jamie Lee of Prince George County was the only rookie entered in 2003. Jamie's conventional-till field of Coker 9704 yielded 71 bu/acre (4,770 kg/ha) after corn. One no-till and two conventional-till fields were included as entries for informational purposes only and not eligible for competition. David Hula of Charles City County produced a no-till field of Renwood 3260 that yielded 82 bu/acre (5,510 kg/ha) after corn. The two conventional fields were grown by Richard Sanford of Westmoreland County. Both fields were grown after a crop of barley/soybeans. The cultivars Pioneer 2643 and Pioneer 2684, respectively, yielded 84 bu/acre (5,644 kg/ha) and 70 bu/acre (4,703 kg/ha).

Success of alternative breeding methods in transferring Fusarium head blight resistance to soft red winter wheat.

J.A. Wilson, C.A. Griffey, J. Chen, D. Nabati, and T. Pridgen.

Objective. Accelerate development of FHB-resistant SRWW cultivars using breeding methods other than traditional topcrossing.

Introduction. The Mid-Atlantic region has suffered significant economic losses in recent years, including 2003, from FHB epidemics (Griffey et al. 1999), reinforcing the need to accelerate development of FHB-resistant cultivars suited to our area. The Virginia Tech Small Grains Program has been involved in developing scab-resistant SRWW cultivars using both traditional and alternative breeding methods. Traditional methods include topcrossing elite parents to obtain an improved cultivar with disease resistance. This method has proven to be successful in developing the scab-resistant Virginia Tech varieties Roane, McCormick, and Tribute. Alternative breeding methods include the transfer of FHB resistance from unadapted germ plasm to adapted elite varieties via backcrossing and the acceleration of breeding progress using the 'wheat x maize' DH system. This paper evaluates progress made to date using such alternative breeding methods.

Materials and methods. Backcrossing. The first crosses between unadapted, scab-resistant lines and adapted elite cultivars were initiated in 1998. Following these initial crosses, a series of one to five backcrosses were made to elite (recurrent) parents. During each of these cycles, the backcrosses were evaluated for scab resistance in a mist-irrigated greenhouse using the single-floret inoculation technique. At various stages of the backcrossing process, populations were developed from selected individuals and planted at Mt. Holly, VA, under mist-irrigated, scab-inoculated conditions. FHB-infected maize seed was the primary inoculum applied to these populations each year. Scab-resistant populations were bulk-selected in early generations and advanced; head selections were made in later generations and evaluated in headrows.

Doubled haploids. The use of the 'wheat/maize' DH system was initiated in 2000 with nine three-way crosses comprised of diverse scab-resistant parents. Emasculated wheat heads were hand-pollinated with maize pollen and immersed in 100 mg/L 2,4-D solution 1 to 2 days later. Embryos were excised 12–16 days after pollination and cultured in test tubes containing nutrient agar medium. The resulting seedlings were then immersed in 0.1 % colchicine solution, rinsed,

transplanted into soil, and vernalized for up to 8 weeks. This process was repeated in 2001 with 10 additional three-way crosses.

Results and discussion. Backcrosses. In 2002, 29 BC₁F₄ and three BC₂F₄ headrows were selected and subsequently evaluated in observation yield tests at two locations and in a FHB nursery in 2003. From these lines, 12 lines were selected and advanced for testing in replicated preliminary yield tests at three locations in 2004. Five of these lines also are being tested in the 2004 Uniform Scab Nurseries. Most of these lines had higher yield and lower FHB incidence than recurrent parent Roane, and four lines had FHB incidence levels lower than recurrent parent Ernie (Wilson et al. 2003). FHB severity and index values followed a similar pattern.

In 2003, 124 backcross lines (28 BC₁F₅, 15 BC₂F₅, 59 BC₂F₄, 3 BC₃F₄, 18 BC₄F₃, and 1 BC₅F₃) were selected as headrows and advanced for evaluation in observation yield tests at two locations and in a FHB-screening nursery in 2004. Field and greenhouse FHB-screening data for the most advanced backcross lines are presented in Table 1. Most of the backcross lines were more resistant to scab than their respective recurrent parents in the field test. In the 2002 greenhouse screening, all of the backcross lines were more resistant than their recurrent parent.

Table 1. Reaction of Fusarium head blight-resistant backcross lines versus recurrent parents in the 2003–04 Virginia Tech Scab Observation Test.

Entry	Pedigree	Field screening (2003)			Greenhouse screening (2002)	
		INC (%)	SEV (%)	IND	SEV (%)	Type-II reading
RECURRENT PARENT	RENWOOD 3260	55	60.0	33.0	47.8	3.9
VA04W-163	W14/5*Renwood 3260, BC ₄ F ₃	10	18.0	1.8	17.2	3.3
VA04W-164	W14/5*Renwood 3260, BC ₄ F ₃	15	25.0	3.8	27.6	3.6
VA04W-165	W14/5*Renwood 3260, BC ₄ F ₃	25	29.0	7.3	20.7	3.4
VA04W-166	W14/5*Renwood 3260, BC ₄ F ₃	15	23.0	3.5	21.4	3.4
VA04W-167	W14/5*Renwood 3260, BC ₄ F ₃	10	21.0	2.1	17.9	3.3
RECURRENT PARENT	ROANE	30	19.0	5.7	39.7	3.9
VA04W-218	W14/5*Roane, BC ₄ F ₃	30	27.0	8.1	11.1	2.7
RECURRENT PARENT	MADISON	75	61.0	46.0	31.9	3.7
VA04W-231	Futai8944/5*Madison, BC ₄ F ₃	55	69.0	38.0	30.0	3.7
VA04W-232	Futai8944/5*Madison, BC ₄ F ₃	50	34.0	17.0	30.0	3.7
VA04W-234	Futai8944/5*Madison,BC ₄ F ₃	55	52.0	29.0	17.1	3.4
RECURRENT PARENT	AGRIPRO MASON	35	36.0	13.0	48.2	4.0
VA04W-239	Shaan85-15 / 6*Agripro Mason, BC ₅ F ₃	50	45.0	23.0	29.4	3.7
RECURRENT PARENT	ERNIE	5	23.0	1.2	44.5	4.0
VA04W-257	Shaan85-2/5*Ernie, BC ₄ F ₃	4	13.3	0.5	22.2	2.9
VA04W-260	VR95B717/5*Ernie, BC ₄ F ₃	20	39.0	7.8	20.7	3.4
VA04W-265	W14 / 5*Ernie, BC ₄ F ₃	5	20.0	1.0	28.1	3.7
VA04W-266	W14 / 5*Ernie, BC ₄ F ₃	5	18.0	0.9	20.8	3.3
VA04W-274	Futai8944 / 5*Ernie, BC ₄ F ₃	4	18.0	0.7	21.7	2.8
VA04W-275	Futai8944 / 5*Ernie, BC ₄ F ₃	10	21.0	2.1	22.9	3.0
VA04W-276	Futai8944 / 5*Ernie, BC ₄ F ₃	4	15.7	0.6	20.7	3.4
VA04W-277	Futai8944 / 5*Ernie, BC ₄ F ₃	20	34.0	6.8	28.0	3.5

Doubled haploids. In 2003, 135 H₃ DH lines were evaluated in inoculated, mist-irrigated greenhouse and field tests. Of these lines, 30 were selected for further evaluation in observation yield tests at two locations and in a FHB-screening nursery during the 2003–04 growing season. Twelve of 19 original three-way crosses were represented among these selections. For most of the lines, scab incidence and severity percentages were 30 or less, and type-II resistance ratings were within the resistant to moderately resistant range (Wilson et al. 2003).

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Wheat projects in 2004.

M.M. Alley and W.E. Thomason.

Current research on wheat management. A survey of the micronutrient content of Virginia wheat is being conducted to determine both the tissue and grain levels associated with major soils used for wheat production. Soil, plant, and grain samples will be analyzed from at least 30 fields. In addition, field trials will be conducted to measure crop response to selected micronutrient applications. Results will be utilized to determine if more detailed research is needed on micronutrient fertilization of wheat as well as to establish a data set of grain micronutrient contents for use by food scientists in assessing the nutritional value of Virginia wheat.

Research on bread wheat quality. Grain yield and yield components of promising bread wheat cultivars, produced using previously determined optimal nitrogen management practices, will be measured at three trials in the state. Seeding rate ranges from below optimum to above optimum populations (15 to 35 seeds/row ft) will be evaluated to determine appropriate seeding rates to optimize yield of bread wheat. These cultivars also will be tested for yield response to foliar fungicide treatments and disease reactions will be assessed in untreated versus fungicide-treated plots. Grain samples will be evaluated for milling and baking quality.

Personnel.

Dr. Daniel E. Brann retired 1 July, 2002, from Virginia Tech following 28 years of devoted service as Small Grains Extension Specialist. Scientists and grain producers alike have benefited from Dan's unwavering commitment and devotion to the small grains industry, and sincere gratitude is expressed to Dan for his outstanding service and leadership. Dan grew up on a grain crop farm in eastern Virginia, obtained a B.S. in Agronomy from Virginia Tech in 1967, and a Ph.D. in Agronomy from West Virginia University in 1971. Dan was employed as the Extension Grain Crops Specialist at Virginia Tech from 1974 until his retirement. During his career he was recognized academically by being promoted to associate and full professor. The most prestigious of his awards include the Statewide Extension Excellence Award and being selected by Progressive Farmer Magazine as 'Man of the Year in Service to Virginia Agriculture'. He is nationally recognized for leadership in research and implementation of intensively managed wheat. Dan conducted the small grains cultivar trials for Virginia Tech and worked very closely with Virginia's small grains breeding program in germ plasm evaluation and strategic planning. He continued to lead the cultivar-testing program and certain aspects of the extension grains position on a volunteer basis until his replacement was hired. He became active in the National Barley Improvement Committee by filling in for Dr. Josa Costa at the Washington Legislative Meeting and Visits in 2003. He is currently vice president of the Virginia Small Grains Association (VSGA) and Chairmen of its Barley Marketing Committee, a member of Virginia Tech's College of Agriculture and Life Sciences Dean's Advisory Council, a member of the Montgomery County Farm Bureau, and a board member of the Virginia Crop Improvement Association. As Chairmen of the VSGA barley marketing committee, he is aggressively developing new markets for hullless barley in the livestock and ethanol industries. He also farms about 500 acres of grain crops with his dad and nephew in eastern Virginia.

Dr. Wade E. Thomason accepted the position of Extension Grain Crops Specialist at Virginia Tech and joined the faculty of the Crop and Soil Environmental Sciences Department in January 2004. Wade is an Oklahoma native and received his B.S. (1996) in animal science, his M.S. (1998) in agronomy, and his Ph.D. (2001) in soil science, all from Oklahoma State University. He comes to Virginia from the Samuel R. Noble Foundation, Ardmore, OK, where he worked as a crop and soil specialist. At Virginia Tech his responsibilities include leading state-wide extension and research programs in production and management of corn, small grains, and sorghum for grain and silage. Wade's extension role is to conduct the statewide corn hybrid testing program and work coöperatively with the small grains breeder to conduct and publish results from the statewide small grain variety testing program. This information is disseminated to growers, industry, and county extension personnel. Wade's research interests include evaluation of profitable cropping systems, evaluations and testing of multiple classes and varieties of wheat and barley for human food, feed, fuel and value added uses, and cultivar selection and fertilization.

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WASHINGTON

USDA-ARS, WHEAT GENETICS, QUALITY, PHYSIOLOGY AND DISEASE RESEARCH UNIT, WASHINGTON STATE UNIVERSITY

361 Johnson Hall, Washington State University, P. O. Box 646430, Pullman, WA 99164-6430, USA.

Stress tolerance genes in wheat, 2003.

Daniel Z. Skinner, Kwang-Hyun Baek, and Brian S. Bellinger.

Manganese superoxide dismutase. The over-expression of the antioxidant enzyme manganese superoxide dismutase (MnSOD) has been shown to confer increased tolerances of environmental stresses in various plants. Using quantitative RT-PCR, we have determined that wheat MnSOD mRNA transcript levels increase rapidly in response to cold temperature and maintain elevated levels of expression through 4 weeks of cold acclimation (Baek and Skinner 2003). We have determined that the wheat genome contains several copies of the MnSOD gene that differ in DNA sequence, some of which express much more strongly in response to cold than others. We are in the process of screening a hexaploid wheat, BAC library for multiple copies of the MnSOD gene in order to elucidate the primary structure of these genes. Knowledge of the molecular structure of the cold responsive MnSOD genes will provide fundamental knowledge on structural characteristics of cold responsive genes.

We developed a method of using quantitative RT-PCR and MnSOD gene primers for quantifying the change in the amount of total RNA following exposure to cold temperature, but is applicable to any treatment. The method was verified using primers for a second gene, phospholipase D (Baek and Skinner 2004).

Evaluation of phospholipid changes during cold acclimation of wheat. Wheat undergoes many changes during the process of cold acclimation, including numerous changes in the levels of phospholipids. We evaluated the levels of 34 phospholipids in a 5-parent diallel cross of winter wheat over a 5-week, cold-acclimation period. Increased concentrations of all phospholipids were measured in response to a 1-week exposure to cold temperature. Some of the phospholipids maintained the elevated expression levels throughout the 5-week period, whereas others declined after the first week of cold exposure. Several differences were found in rates of accumulation and loss among the different populations.

Statistical analysis of the diallel data is expected to provide information on the genetic control of phospholipid accumulation and loss during cold acclimation.

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Epidemiology and control of wheat stripe rust in the United States, 2003.

Xianming Chen, Paul Ling, David A. Wood, Mary K. Moore, and Vihanga Pahalawatta.

Monitoring rusts, predicting epidemics, assessing yield losses, and identifying races of *Puccinia striiformis* f. sp. *tritici*. Wheat stripe rust, leaf rust, and stem rust were monitored throughout the Pacific Northwest (PNW) using trap plots and field survey. The diseases were accurately predicted for the PNW in 2003 using monitoring data and predictive models based on environmental factors such as temperature, precipitations, and resistance of wheat cultivars. Through coöperators in many other states, wheat stripe rust was monitored throughout the United States. In 2003, wheat stripe rust occurred in more than 25 states from Washington State to Florida and from Texas to Ontario, Canada. Severe yield losses caused by stripe rust occurred in the PNW, California, Texas, Louisiana, Arkansas, Oklahoma, Kansas, Nebraska, Colorado, and South Dakota. In 2003, stripe rust epidemic caused wheat yield losses of 88.88 million bushels plus multimillion dollars on fungicide application in the United States.

In the PNW, wheat stripe rust occurred earlier than normal on winter wheat and spread quickly on spring wheat in 2003. The dry weather conditions from early June slowed the epidemic development. Foliar application of fungicides in the fields of susceptible winter and spring wheat cultivars prevented major yield losses. The impact of the epidemic was assessed based on rust severities and yield losses of major cultivars in the experimental plots and rust survey in commercial fields. In the state of Washington, stripe rust caused 1.5 % yield loss of winter wheat production and 3.5 % yield loss of spring wheat production. The widely grown winter wheat cultivars such as Eltan, Madsen, Rod, and Stephens, and spring wheat cultivars like Alpowa, which have various levels of high-temperature, adult-plant (HTAP) resistance, prevented the most devastating epidemic that could have occurred if the resistant cultivars had not been grown. Widely grown resistant cultivars and use of fungicides in fields grown with susceptible cultivars reduced yield losses to 3.1 million bushels (1.1 %) in the PNW. In 2003, wheat leaf rust was severe in the northwest of Washington but was light in the major wheat production areas in eastern Washington, and stem rust was absent due to the dry weather conditions from early June. The nurseries of single-gene lines with leaf rust and stem rust resistance genes were covered with stripe rust. Leaf and stem rusts did not cause significant yield losses in the PNW.

More than 400 wheat stripe rust samples from wheat fields and grasses collected in the PNW and sent by cooperators throughout the US were evaluated to determine their virulence. These samples were increased on susceptible cultivars and tested on a set of 20 wheat genotypes that are used to differentiate races of *P. striiformis* f. sp. *tritici* in the US. From the collections, 25 previously identified and 13 new races were detected. Of the 38 races, only eight (PST-77, 78, 79, 80, 97, 98, 99, and 100) had frequencies more than 1 %. The eight races that counted for 89.9 % of the collections belong to a group of races with common virulences on Lemhi, Lee, Fielder, Express, Yr8, Yr9, Clement, and Compair). The group of the races were first detected in 2000 and caused severe epidemics from 2000 to 2003 in the US. In 2003, races PST-98 (virulent on Lemhi, Heines VII, Produra, Stephens, Lee, Fielder, Express, Yr8, Yr9, Clement, and Compair) and PST-100 (virulent on Lemhi, Heines VII, Produra, Yamhill, Stephens, Lee, Fielder, Express, Yr8, Yr9, Clement, and Compair) were the most predominant, each of these two races counting for 29.5 % of the samples throughout the United States.

Leaf rust samples were collected and sent to the Cereal Disease Laboratory in the University of Minnesota. In 2003, two races, MBGJ (virulent on *Lr1*, *Lr3a*, *Lr11*, *Lr10*, and *Lr14a*) and MCDS (virulent on *Lr1*, *Lr3a*, *Lr26*, *Lr17*, *LrB*, *Lr10*, and *Lr14a*) were detected in the PNW. Race MBGJ occurred previously in 2002.

Evaluating wheat germ plasm and breeding lines for resistance to rusts and other foliar diseases. In 2003, we evaluated more than 13,000 winter and spring wheat entries including germ plasm, genetic populations, and breeding

lines from the National Germplasm Collection Center and wheat breeders in the greenhouse for resistance to selected predominant stripe rust races and/or at various field sites for resistance to naturally occurring races. The wheat entries also were evaluated for resistance to leaf rust, powdery mildew, and physiological leaf spot in field sites where these diseases occurred naturally. Germ plasms and breeding lines with resistance to the disease especially stripe rust were identified. We have provided the information to breeders for developing resistant cultivars. Germ plasms were selected for further characterization of resistance and used to develop adapted lines for determine virulence of the stripe rust population and for breeding programs to develop cultivars with superior resistance.

Determining genetics of resistance and develop molecular markers for stripe rust resistance genes. To develop adapted resistant germ plasms, determine genetics of resistance, and develop molecular markers for genes conferring resistance to stripe rust, crosses and backcrosses were made with Alpowa, Express, IDO377s, Zak, *Yr5*, *Yr15*, *Yr18*, and Avocet Susceptible (AVS) in the field and greenhouse. Alpowa and Express have different levels of durable HTAP resistance to stripe rust. IDO377s has high level seedling resistance against predominant races. Zak has high-level seedling resistance that is no longer effective against new races. The *Yr5* and *Yr15* NILs with the stripe rust resistance gene *Yr5* and *Yr15*, respectively, in the AVS background are resistant to all races of the stripe rust pathogen identified so far in the US. The *Yr18* resistance, also in the AVS background, is not race specific and durable. Crosses of Alpowa, Express, IDO377s, and Zak with AVS are used to identify and map genes in these cultivars for stripe rust resistance. Crosses of Alpowa with Express are used to combine genes for HTAP resistance from each of the cultivars to obtain high-level resistance. Crosses of Zak with Alpowa and Express are used to incorporate HTAP resistance into the Zak background. Crosses of Alpowa and Zak with the *Yr5*, *Yr15*, and *Yr18* NILs are used to incorporate these effective genes for all-stage (seedling) or HTAP resistance into Alpowa and Zak to improve the Alpowa resistance. F₃ and BC₁ generations have been obtained for these crosses and are currently used in genetic studies and molecular mapping of resistance genes in these cultivars.

We have developed user-friendly markers for the *Yr5* gene. These markers are used in MAS to incorporate the *Yr5* resistance into commercial cultivars in several breeding programs and used in our program to clone *Yr5* for elucidating resistance mechanisms. We also have developed molecular markers for *Yr15*. Collaborating with the Campbell and Kidwell labs, we are using the markers to determine presence or absence of *Yr15* in breeding lines and to combine both *Yr5* and *Yr15* into elite breeding lines.

Through collaboration with Ed Souza at the University of Idaho, we evaluated a genetic population of recombinant inbred lines developed from a cross between wheat varieties IDO444 and Rio Blanc and identified genes for all-stage (seedling) and HTAP resistance to stripe rust. The resistance genes are potentially new and should be useful for breeding resistance to stripe rust.

Stephens is the major source for durable HTAP resistance that has been used in the breeding programs in the PNW and has started to used in the other regions. We have identified molecular markers for genes conferring the all-stage (seedling) resistance and some of the genes conferring the durable HTAP resistance. To diversify sources of durable resistance used in breeding programs in the PNW and other regions, we have also initiated molecular mapping study on Druchamp that has a higher level of HTAP resistance than Stephens and its HTAP resistance is conferred by different genes.

Wheat is generally resistant to the barley stripe rust pathogen and barley is generally resistant to the wheat stripe rust pathogen. Therefore, wheat can be a great source of resistance to barley stripe rust and vice versa. However, genetic basis of these so-called non-host resistances have not been determined. We have made wheat and barley crosses to genetically characterize the resistances. Based on segregation of F₂, F₃, and backcross progeny tested with selected races, we found that a single dominant gene in Lemhi wheat confers resistance to barley stripe rust and two genes (one dominant and one recessive) in 'Steptoe' barley conferring resistance to wheat stripe rust. With 11 resistance gene analog polymorphism (RGAP) markers, we mapped the wheat gene on chromosome 1B close to but different from *Yr21*, previously identified in our lab. A linkage group with 12 RGAP markers was constructed for the dominant gene in Steptoe for resistance to wheat stripe rust. The study provides scientific basis to utilize genes in barley for resistance to races of wheat stripe rust and vice versa.

Constructing a hexaploid wheat BAC library for cloning genes for resistance to stripe rust. A genomic BAC library of common wheat has been constructed using the wheat *Yr5* line. The BAC library consists of 410,000 clones with an average insert size of 130 kb and covers approximately 3.3x wheat genome equivalents. Colony pools and high-

density filters of the BAC library have been made for identifying resistance clones. Molecular markers specific to the *Yr5* resistance gene were used to screen the multidimensional BAC clone pools. To isolate the expressed sequences from the candidate regions, a cDNA library from the *Yr5* line was constructed and is screened with candidate regions as a probe. The wheat BAC library will be used to clone other genes for stripe rust resistance and study of wheat genomics.

Determining the effectiveness and use of foliar fungicides for rust control. Fungicides were evaluated for controlling stripe rust in spring wheat plots near Pullman, WA. Wheat cultivars Zak and Fielder were planted on 27 April, 2003. Eight fungicide treatments were conducted on 2 July at the flowering stage. Plots for untreated checks were not sprayed. A randomized block design was used with four replications for each treatment. Data on stripe rust severity (percent foliage with stripe rust) were recorded on 2 July before fungicide application and on 17 July at late milk stage. Yields were determined from plots harvested in 18 August. All the fungicide treatments effectively reduced stripe rust severity. All treatment except Quadris applied at 6.1 fl oz/acre significantly increased grain yield compared to the non-treated check on Fielder; and a new fungicide formulation (A13705 SC 200) applied at the rate of 13.7 fl oz/acre significantly increased grain yield on Zak.

Cultivars with various levels of resistance respond differently to fungicide applications. To determine whether it is worthy to apply fungicides on various cultivars, 23 winter wheat and 16 spring wheat cultivars grown in the western U.S. that had not been previously tested for fungicide control were tested in randomized split-block experiments with four replicates near Pullman, WA, in 2003. When highly susceptible cultivars had 10 % stripe rust, a half of a plot was sprayed with Quadris and the other half was not sprayed. Without fungicide application, seven moderately susceptible and susceptible winter wheat cultivars had yield losses ranging from 14 % to 34 %; nine moderately susceptible and susceptible spring wheat cultivars had yield losses from 11 % to 32 %. Fungicide application increased yields by 16–52 %. Fields of these cultivars should be sprayed with fungicides. Five winter and two spring cultivars with moderate level of resistance had yield losses of 5–12 %. Fungicide spray increased yields by 6–14 %. Fungicide application for these cultivars should be determined based on yield potential in various regions. Eleven winter and five spring wheat cultivars of resistance didn't have significant differences in yield between fungicide treated and non-treated blots. The information is useful for growers to make maximum profit by using fungicides and also reduce unnecessary use of fungicides.

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USDA-ARS WESTERN WHEAT QUALITY LABORATORY
E-202 Food Science & Human Nutrition Facility East, Washington State University,
Pullman, WA 99164, USA.
www.wsu.edu/~wwql/php/index.php

Craig F. Morris, A.D. Bettge, D.A. Engle, M.L. Baldrige, R.L. Engle, G.E. King, G.L. Jacobson, A.N. Massa, I. Eujayl, E.P. Fuerst, K.R. Gedye, C.C. Burke, P. Greenwell, H. Tanaka, W.J. Kelley, M.J. Freston, P.K. Boyer, L. Nguyen, E.E. Galli, S.M. Finnie, E. Wagner, S.M. Leach, and Y. Haruta.

The mission of the lab is two-fold: conduct milling, baking, and end-use quality evaluations on wheat breeding lines, and conduct research on wheat grain quality and utilization. The lab continues to move into web-based information transfer and has added extensive enhancements to our web site: <http://www.wsu.edu/~wwql/php/index.php>. To provide greater access to our research, we developed a database of wheat varieties relating kernel hardness and puroindoline allele. We are in the process of placing our research publications on our web site.

We are serving as curator of the grain hardness, puroindoline, and *Gsp-1* gene sections of the Catalogue of Gene Symbols in Wheat. Several new alleles have been documented in *Ae. tauschii*, synthetic hexaploids from CIMMYT, and other diploid taxa.

We are in the process of establishing the Sino-U.S. Joint Centers for Wheat Quality and Pathology in collaboration with Dr. He, CIMMYT-Beijing, and the Institute of Crop Breeding and Cultivation, Chinese Academy of Agricultural Sciences, USDA-ARS, and Washington State University.

C.F. Morris and D.A. Engle lead the Pacific Northwest Wheat Quality Council, a consortium of collaborators who evaluate the quality of new cultivars and advanced breeding lines.

A.D. Bettge currently serves as chairman of the AACC Soft Wheat and Flour Technical Committee. New methodology for the analysis of end-use characteristics of wheat is studied by this committee for inclusion in the AACCs Approved Methods manual. Recent methods that have been studied collaboratively and approved include, i) Solvent Retention Capacity (SRC), which estimates a number of end-use quality factors such as protein quality, starch damage and pentosan content, and ii) Flour Swelling Volume (FSV), which measures starch swelling and the impact of granule-bound starch synthase allelic state. An L-DOPA substrate-based method for estimation of polyphenol oxidase content of wheat, a contributor to Asian noodle discoloration has been submitted for approval and inclusion in the Approved Methods manual.

C.F. Morris was awarded an OECD fellowship and will spend 6 weeks in the laboratory of Dr. Zoltan Bedö, Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvasar, Hungary.

Postdoctoral research associates include A.N. Massa, I. Eujayl, E.P. Fuerst, K.R. Gedye, and C.C. Burke; visiting scientists are P. Greenwell and H. Tanaka; and Y. Haruta is a visitor from a Japanese milling company.

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